

SeqCore version 4.5
Copyright (c) 1993 - 1998 CompuGen Ltd.

OM protein : protein search, using SW model

Run on: June 22, 1999, 10:59:47 ; Search time 45.16 Seconds

(without alignments)
93,311 Million cell updates/sec

Title: US-09-030-061-7

RefSeq score: 812

Sequence: 1 NGRHTTAVRININDVL KKDENGKSVPTLNLHQS 157

Scoring table: BLOSUM62

Database: SwissProt_36*

Fried. No. is the number of results predicted by chance to have a
score higher than the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Match	Length	DB ID	Description
1	812	100.0	192	IL18_MOUSE	P70380 mus musculus
2	742.5	91.4	194	IL18_RAT	P97636 rattus norv
3	520	64.0	193	IL18_HUMAN	Q14116 homo sapien
4	362	48.6	160	IL18_PIG	Q19073 sus scrofa
5	83.5	10.3	803	IL18_PIG	P43864 haemophilus
6	81	10.0	267	IL18_PIG	P28899 sus scrofa
7	80.5	9.4	526	IL18_PIG	Q00952 stichococ
8	80	9.4	1196	IL18_PIG	P46081 stichococ
9	79.5	9.8	167	IL18_PIG	Q58219 methanococ
10	76	9.7	266	IL18_BOVIN	P09428 bos taurus
11	78.5	9.7	270	IL18_MOUSE	P01582 mus musculu
12	78.5	9.7	604	IL18_MOUSE	P34283 saccharomyc
13	77.5	9.5	270	IL18_PIG	P18430 sus scrofa
14	77.5	9.5	439	IL18_PIG	Q58221 methanococ
15	76.5	9.4	621	IL18_PIG	P56116 haemophilus
16	76.5	9.4	695	IL18_PIG	P45806 haemophilus
17	75	9.2	269	IL18_MOUSE	P48090 macaca mula
18	75	9.2	269	IL18_MOUSE	P51493 macaca mela
19	75	9.2	269	IL18_MOUSE	P21621 ovis aries
20	74.5	9.2	269	IL18_MOUSE	P01584 homo sapien
21	74	9.1	269	IL18_MOUSE	P70382 homo sapien
22	74	9.1	1082	IL18_MOUSE	Q08999 homo sapien
23	74	9.1	972	IL18_MOUSE	P25191 porcula por
24	74	9.1	624	IL18_MOUSE	Q10198 schistosac
25	74	9.1	624	IL18_MOUSE	P28166 schistosac
26	73	9.0	541	IL18_MOUSE	P44973 haemophilus
27	73	9.0	541	IL18_MOUSE	Q08854 haemophilus
28	72.5	8.9	541	IL18_MOUSE	Q50327 mycoplasma
29	72	8.9	611	IL18_MOUSE	P32769 saccharomyc
30	72	8.9	611	IL18_MOUSE	P35845 saccharomyc
31	72	8.9	611	IL18_MOUSE	P35845 saccharomyc
32	71.5	8.7	267	IL18_MOUSE	P29986 saccharomyc
33	71	8.7	267	IL18_MOUSE	P29986 saccharomyc
34	71	8.7	267	IL18_MOUSE	P29986 saccharomyc
35	71	8.7	267	IL18_MOUSE	P29986 saccharomyc
36	71	8.7	267	IL18_MOUSE	P29986 saccharomyc
37	71	8.7	267	IL18_MOUSE	P29986 saccharomyc
38	70.5	8.7	267	IL18_MOUSE	P29986 saccharomyc
39	70.5	8.7	267	IL18_MOUSE	P29986 saccharomyc
40	70.5	8.7	267	IL18_MOUSE	P29986 saccharomyc
41	70.5	8.7	267	IL18_MOUSE	P29986 saccharomyc
42	70.5	8.7	267	IL18_MOUSE	P29986 saccharomyc
43	70.5	8.7	267	IL18_MOUSE	P29986 saccharomyc

ALIGNMENTS

RESULT	1	2
IL18_MOUSE	STANDARD	PRT
AC	P70380	192 AA
DT	15-JUL-1998 (REL. 36, CREATED)	
DT	15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)	
DT	15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)	
DE	INTERLEUKIN-18 PREPROPEP (11-18) (INTERFERON-GAMMA INDUCING FACTOR)	
DE	(IFN-GAMMA-INDUCING FACTOR) (INTERLEUKIN-1 GAMMA) (IL-1 GAMMA).	
OS	IL18 OR IGIF.	
OS	MUS MUSCULUS (MUS).	
CC	ETRAVITIA: METACOA: IFFERATA: VERIFERATA: IFFERATA: MAMMALIA:	
CC	ETRAVITIA: RODENTIA:	
RN	(1)	
PP	SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.	
PP	TISSUE=LIVER.	
FX	MEDLINE: 96061009.	
RA	OKAMURA H., ISHII H., KOMATSU T., YUJISHIRO M., HAKURA A.,	
RA	TANIMOTO T., TORIJOE Y., OKURA T., NITADA Y., HATSUBI K.,	
RA	AKITA K., NAKABA M., TANABE F., KONISHI K., FUKUDA S., KORIYAMA M.,	
RL	NATURE 378:88-91(1995).	
SN	(2)	
RP	SEQUENCE OF 1-191 FROM N.A.	
RC	STRAIN=NDU; TISSUE=PANCREAS;	
FX	MEDLINE: 97174346.	
RA	ROTH H., JENKINS N.A., COVELAND N.G., KOUB H.,	
RL	J. CLIN. INVEST. 94:469-474(1997).	
CC	FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEN CELL	
CC	AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE 1	
CC	CELLS.	
OP	EMBL: U06444; GI:449337.	
DR	EXPL. 060444; S1501735.	
DR	MOL. MBI:107846; IGIF.	
KT	CYTOKINE.	
FT	PROPEP 1 35	
FT	CHAIN 36 192	
FT	CONFLICT 182 185	
FT	CONFLICT 182 185	
SE	SEQUENCE 192 AA; 28739 MW; 46320876 Da; 3737.	
Query Match	100.0% Score 812; DB 1; Length 192;	
Host Local Similarity	100.0% (E=0.0); E=0.0; L=192;	
Matches	157; Conserving 0; Mismatches 0; Indels 0; Gaps	
1	NGRHTTAVRININDVLFPFPLVFLKLTINLHQS 157	
2	NGRHTTAVRININDVLFPFPLVFLKLTINLHQS 157	
3	NGRHTTAVRININDVLFPFPLVFLKLTINLHQS 157	
4	NGRHTTAVRININDVLFPFPLVFLKLTINLHQS 157	
5	NGRHTTAVRININDVLFPFPLVFLKLTINLHQS 157	
6	NGRHTTAVRININDVLFPFPLVFLKLTINLHQS 157	
7	NGRHTTAVRININDVLFPFPLVFLKLTINLHQS 157	
8	NGRHTTAVRININDVLFPFPLVFLKLTINLHQS 157	
9	NGRHTTAVRININDVLFPFPLVFLKLTINLHQS 157	
10	NGRHTTAVRININDVLFPFPLVFLKLTINLHQS 157	
11	NGRHTTAVRININDVLFPFPLVFLKLTINLHQS 157	
12	NGRHTTAVRININDVLFPFPLVFLKLTINLHQS 157	
13	NGRHTTAVRININDVLFPFPLVFLKLTINLHQS 157	
14	NGRHTTAVRININDVLFPFPLVFLKLTINLHQS 157	
15	NGRHTTAVRININDVLFPFPLVFLKLTINLHQS 157	
16	NGRHTTAVRININDVLFPFPLVFLKLTINLHQS 157	
17	NGRHTTAVRININDVLFPFPLVFLKLTINLHQS 157	
18	NGRHTTAVRININDVLFPFPLVFLKLTINLHQS 157	
19	NGRHTTAVRININDVLFPFPLVFLKLTINLHQS 157	
20	NGRHTTAVRININDVLFPFPLVFLKLTINLHQS 157	
21	NGRHTTAVRININDVLFPFPLVFLKLTINLHQS 157	
22	NGRHTTAVRININDVLFPFPLVFLKLTINLHQS 157	
23	NGRHTTAVRININDVLFPFPLVFLKLTINLHQS 157	
24	NGRHTTAVRININDVLFPFPLVFLKLTINLHQS 157	
25	NGRHTTAVRININDVLFPFPLVFLKLTINLHQS 157	
26	NGRHTTAVRININDVLFPFPLVFLKLTINLHQS 157	
27	NGRHTTAVRININDVLFPFPLVFLKLTINLHQS 157	
28	NGRHTTAVRININDVLFPFPLVFLKLTINLHQS 157	
29	NGRHTTAVRININDVLFPFPLVFLKLTINLHQS 157	
30	NGRHTTAVRININDVLFPFPLVFLKLTINLHQS 157	
31	NGRHTTAVRININDVLFPFPLVFLKLTINLHQS 157	
32	NGRHTTAVRININDVLFPFPLVFLKLTINLHQS 157	
33	NGRHTTAVRININDVLFPFPLVFLKLTINLHQS 157	
34	NGRHTTAVRININDVLFPFPLVFLKLTINLHQS 157	
35	NGRHTTAVRININDVLFPFPLVFLKLTINLHQS 157	
36	NGRHTTAVRININDVLFPFPLVFLKLTINLHQS 157	
37	NGRHTTAVRININDVLFPFPLVFLKLTINLHQS 157	
38	NGRHTTAVRININDVLFPFPLVFLKLTINLHQS 157	
39	NGRHTTAVRININDVLFPFPLVFLKLTINLHQS 157	
40	NGRHTTAVRININDVLFPFPLVFLKLTINLHQS 157	
41	NGRHTTAVRININDVLFPFPLVFLKLTINLHQS 157	
42	NGRHTTAVRININDVLFPFPLVFLKLTINLHQS 157	
43	NGRHTTAVRININDVLFPFPLVFLKLTINLHQS 157	

IMMUNITY

AC	P43854	01-NEW-1066 (PBT)	33	CONTAMINANT
AC	P43854	01-NEW-1066 (PBT)	33	CONTAMINANT

01-NOV-1995	(REL. 32, CREATED)
01-NOV-1995	(REL. 32, LAST SEQUENCE UPDATE)

1. 1971. MARCH 30. 9 AM. STAFF 30. DB 1. Length 1960.
 2. 1971. JULY 31. STAFF 29. 24 AM. Prod. No. 14.
 3. 1971. SEPTEMBER 30. 24 AM. Mismatch 57. Index 28. Gaps 4.
 4. 1971. DECEMBER 31. STAFF 28. 24 AM. Mismatch 57. Index 28. Gaps 4.
 5. 1972. JANUARY 31. STAFF 27. 24 AM. Mismatch 57. Index 28. Gaps 4.
 6. 1972. FEBRUARY 29. STAFF 26. 24 AM. Mismatch 57. Index 28. Gaps 4.
 7. 1972. MARCH 31. STAFF 25. 24 AM. Mismatch 57. Index 28. Gaps 4.
 8. 1972. APRIL 30. STAFF 24. 24 AM. Mismatch 57. Index 28. Gaps 4.
 9. 1972. MAY 31. STAFF 23. 24 AM. Mismatch 57. Index 28. Gaps 4.
 10. 1972. JUNE 30. STAFF 22. 24 AM. Mismatch 57. Index 28. Gaps 4.
 11. 1972. JULY 31. STAFF 21. 24 AM. Mismatch 57. Index 28. Gaps 4.
 12. 1972. AUGUST 31. STAFF 20. 24 AM. Mismatch 57. Index 28. Gaps 4.
 13. 1972. SEPTEMBER 30. STAFF 19. 24 AM. Mismatch 57. Index 28. Gaps 4.
 14. 1972. OCTOBER 31. STAFF 18. 24 AM. Mismatch 57. Index 28. Gaps 4.
 15. 1972. NOVEMBER 30. STAFF 17. 24 AM. Mismatch 57. Index 28. Gaps 4.
 16. 1972. DECEMBER 31. STAFF 16. 24 AM. Mismatch 57. Index 28. Gaps 4.
 17. 1973. JANUARY 31. STAFF 15. 24 AM. Mismatch 57. Index 28. Gaps 4.
 18. 1973. FEBRUARY 29. STAFF 14. 24 AM. Mismatch 57. Index 28. Gaps 4.
 19. 1973. MARCH 31. STAFF 13. 24 AM. Mismatch 57. Index 28. Gaps 4.
 20. 1973. APRIL 30. STAFF 12. 24 AM. Mismatch 57. Index 28. Gaps 4.
 21. 1973. MAY 31. STAFF 11. 24 AM. Mismatch 57. Index 28. Gaps 4.
 22. 1973. JUNE 30. STAFF 10. 24 AM. Mismatch 57. Index 28. Gaps 4.
 23. 1973. JULY 31. STAFF 9. 24 AM. Mismatch 57. Index 28. Gaps 4.
 24. 1973. AUGUST 31. STAFF 8. 24 AM. Mismatch 57. Index 28. Gaps 4.
 25. 1973. SEPTEMBER 30. STAFF 7. 24 AM. Mismatch 57. Index 28. Gaps 4.
 26. 1973. OCTOBER 31. STAFF 6. 24 AM. Mismatch 57. Index 28. Gaps 4.
 27. 1973. NOVEMBER 30. STAFF 5. 24 AM. Mismatch 57. Index 28. Gaps 4.
 28. 1973. DECEMBER 31. STAFF 4. 24 AM. Mismatch 57. Index 28. Gaps 4.
 29. 1974. JANUARY 31. STAFF 3. 24 AM. Mismatch 57. Index 28. Gaps 4.
 30. 1974. FEBRUARY 29. STAFF 2. 24 AM. Mismatch 57. Index 28. Gaps 4.
 31. 1974. MARCH 31. STAFF 1. 24 AM. Mismatch 57. Index 28. Gaps 4.
 32. 1974. APRIL 30. STAFF 0. 24 AM. Mismatch 57. Index 28. Gaps 4.
 33. 1974. MAY 31. STAFF -1. 24 AM. Mismatch 57. Index 28. Gaps 4.
 34. 1974. JUNE 30. STAFF -2. 24 AM. Mismatch 57. Index 28. Gaps 4.
 35. 1974. JULY 31. STAFF -3. 24 AM. Mismatch 57. Index 28. Gaps 4.
 36. 1974. AUGUST 31. STAFF -4. 24 AM. Mismatch 57. Index 28. Gaps 4.
 37. 1974. SEPTEMBER 30. STAFF -5. 24 AM. Mismatch 57. Index 28. Gaps 4.
 38. 1974. OCTOBER 31. STAFF -6. 24 AM. Mismatch 57. Index 28. Gaps 4.
 39. 1974. NOVEMBER 30. STAFF -7. 24 AM. Mismatch 57. Index 28. Gaps 4.
 40. 1974. DECEMBER 31. STAFF -8. 24 AM. Mismatch 57. Index 28. Gaps 4.
 41. 1975. JANUARY 31. STAFF -9. 24 AM. Mismatch 57. Index 28. Gaps 4.
 42. 1975. FEBRUARY 29. STAFF -10. 24 AM. Mismatch 57. Index 28. Gaps 4.
 43. 1975. MARCH 31. STAFF -11. 24 AM. Mismatch 57. Index 28. Gaps 4.
 44. 1975. APRIL 30. STAFF -12. 24 AM. Mismatch 57. Index 28. Gaps 4.
 45. 1975. MAY 31. STAFF -13. 24 AM. Mismatch 57. Index 28. Gaps 4.
 46. 1975. JUNE 30. STAFF -14. 24 AM. Mismatch 57. Index 28. Gaps 4.
 47. 1975. JULY 31. STAFF -15. 24 AM. Mismatch 57. Index 28. Gaps 4.
 48. 1975. AUGUST 31. STAFF -16. 24 AM. Mismatch 57. Index 28. Gaps 4.
 49. 1975. SEPTEMBER 30. STAFF -17. 24 AM. Mismatch 57. Index 28. Gaps 4.
 50. 1975. OCTOBER 31. STAFF -18. 24 AM. Mismatch 57. Index 28. Gaps 4.
 51. 1975. NOVEMBER 30. STAFF -19. 24 AM. Mismatch 57. Index 28. Gaps 4.
 52. 1975. DECEMBER 31. STAFF -20. 24 AM. Mismatch 57. Index 28. Gaps 4.
 53. 1976. JANUARY 31. STAFF -21. 24 AM. Mismatch 57. Index 28. Gaps 4.
 54. 1976. FEBRUARY 29. STAFF -22. 24 AM. Mismatch 57. Index 28. Gaps 4.
 55. 1976. MARCH 31. STAFF -23. 24 AM. Mismatch 57. Index 28. Gaps 4.
 56. 1976. APRIL 30. STAFF -24. 24 AM. Mismatch 57. Index 28. Gaps 4.
 57. 1976. MAY 31. STAFF -25. 24 AM. Mismatch 57. Index 28. Gaps 4.
 58. 1976. JUNE 30. STAFF -26. 24 AM. Mismatch 57. Index 28. Gaps 4.
 59. 1976. JULY 31. STAFF -27. 24 AM. Mismatch 57. Index 28. Gaps 4.
 60. 1976. AUGUST 31. STAFF -28. 24 AM. Mismatch 57. Index 28. Gaps 4.
 61. 1976. SEPTEMBER 30. STAFF -29. 24 AM. Mismatch 57. Index 28. Gaps 4.
 62. 1976. OCTOBER 31. STAFF -30. 24 AM. Mismatch 57. Index 28. Gaps 4.
 63. 1976. NOVEMBER 30. STAFF -31. 24 AM. Mismatch 57. Index 28. Gaps 4.
 64. 1976. DECEMBER 31. STAFF -32. 24 AM. Mismatch 57. Index 28. Gaps 4.
 65. 1977. JANUARY 31. STAFF -33. 24 AM. Mismatch 57. Index 28. Gaps 4.
 66. 1977. FEBRUARY 29. STAFF -34. 24 AM. Mismatch 57. Index 28. Gaps 4.
 67. 1977. MARCH 31. STAFF -35. 24 AM. Mismatch 57. Index 28. Gaps 4.
 68. 1977. APRIL 30. STAFF -36. 24 AM. Mismatch 57. Index 28. Gaps 4.
 69. 1977. MAY 31. STAFF -37. 24 AM. Mismatch 57. Index 28. Gaps 4.
 70. 1977. JUNE 30. STAFF -38. 24 AM. Mismatch 57. Index 28. Gaps 4.
 71. 1977. JULY 31. STAFF -39. 24 AM. Mismatch 57. Index 28. Gaps 4.
 72. 1977. AUGUST 31. STAFF -40. 24 AM. Mismatch 57. Index 28. Gaps 4.
 73. 1977. SEPTEMBER 30. STAFF -41. 24 AM. Mismatch 57. Index 28. Gaps 4.
 74. 1977. OCTOBER 31. STAFF -42. 24 AM. Mismatch 57. Index 28. Gaps 4.
 75. 1977. NOVEMBER 30. STAFF -43. 24 AM. Mismatch 57. Index 28. Gaps 4.
 76. 1977. DECEMBER 31. STAFF -44. 24 AM. Mismatch 57. Index 28. Gaps 4.
 77. 1978. JANUARY 31. STAFF -45. 24 AM. Mismatch 57. Index 28. Gaps 4.
 78. 1978. FEBRUARY 29. STAFF -46. 24 AM. Mismatch 57. Index 28. Gaps 4.
 79. 1978. MARCH 31. STAFF -47. 24 AM. Mismatch 57. Index 28. Gaps 4.
 80. 1978. APRIL 30. STAFF -48. 24 AM. Mismatch 57. Index 28. Gaps 4.
 81. 1978. MAY 31. STAFF -49. 24 AM. Mismatch 57. Index 28. Gaps 4.
 82. 1978. JUNE 30. STAFF -50. 24 AM. Mismatch 57. Index 28. Gaps 4.
 83. 1978. JULY 31. STAFF -51. 24 AM. Mismatch 57. Index 28. Gaps 4.
 84. 1978. AUGUST 31. STAFF -52. 24 AM. Mismatch 57. Index 28. Gaps 4.
 85. 1978. SEPTEMBER 30. STAFF -53. 24 AM. Mismatch 57. Index 28. Gaps 4.
 86. 1978. OCTOBER 31. STAFF -54. 24 AM. Mismatch 57. Index 28. Gaps 4.
 87. 1978. NOVEMBER 30. STAFF -55. 24 AM. Mismatch 57. Index 28. Gaps 4.
 88. 1978. DECEMBER 31. STAFF -56

RX MEDLINE: 89016591.
CA LEONE S.P., FIASCHI G.M., LAWMAN M., GRAY P.W.
RL NUCLEIC ACIDS RES. 16:9054-9054(1988).
RN [2]


```

01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
HEAT SHOCK PROTEIN HSPA (HIGH TEMPERATURE PROTEIN G) .
HSPG OR HP0210 .
HELICORATER PYLOPI (CAMPELACIATER PYLOPI) .
PROKARYOTA: GRAM-NEGATIVE: SPOTOCHACTERIA:
APPROXIT. MOTILE. HELICAL ANTERIOR VIBRIOID.
[1]
SEQUENCE FROM N.A.
RP STRAIN-26695:
RX MEDLINE: 9724447.
TOMR T -P. WHITE O. KFLAVAGE A P, CLAYTON P A, SUTTON G G,
RA FEISCHSMANN P D, KETCHUM K A, KLENK H -P, GILL S, DOUGHERTY B A,
RA NELSON K, STARKENBRUSH J, ZHOU L, KIPKRESS F F, PETERSON S,
RA LOTTOUS B, RICHARDSON P, LINDSON P, KHALAK H G, GLOERK A,
RA MCKENNEY K, FITZGERALD L M, LEE N, ADAMS M D, HICKEY E K,
RA BENG D E, JOYAVNE J D, UTERBACK T R, PETERSON J D, KELLEY J M,
RA COTTON M F, WEIDMAN J W, FRITZ C, BOWMAN G, WATHEY L, WALLIN E,
RA HATES W S, ROBINSON S M, FAAP P D, SMITH H O, FRASER C M,
RA VENTER J C,
RL NATURE 386:539-547(1997) .
CC -1- FUNCTION: MOLECULAR CHAPERONE. HAS ATPASE ACTIVITY
CC (BY SIMILARITY)
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.
DR EMBL: AEO00541: G213300: -
DR HIGR: HP0210: -
ER PROSITE: PSC0296: HSP90: 1.
KW CHAPERONE, ATP-BINDING, HEAT SHOCK
NC SEQUENCE: 621 AA, 72774 MW, 234AD59 CNO3:

```

```

Query: March 19 48: Score 76.5: DB 1: Length 621;
      Post local similarity: 33.0%: Prod No. 13;
      Matched 28 100% identity 21 Mismatches 52, Indels 17, Gaps 4
01 12 MTDGDAEAEDEGRLTYMHYRSEVAGLAVILSVK---DSKMSILDSCKNKLIIFSEEDMP 88
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
02 31 LPEVYSASDAELKINVMIMDEKILKGLNTPTSHLSPLDSCKLTITKIDNSIGDKNDLI 90
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
03 07 ENIDCTQSLLIFFOKRVPOHNM-----DEESSLYGCHFLAOCKEDDAPKILLKKDE 141
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
04 01 EHTTAKSGGKKNLSLSLSDEKKEKSAIIGDGVGFVAFVAVS-----KIYVOTKKV 143
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
05 07 142 MGDKS 146
   :: ::
06 144 NSDOA 148

```

Search completed. Time 22: 1999, 10:59.48
Job time: 74 sec

100

101

102

103

104

105

106

107

108

109

110

111

112

113

114

115

116

117

118

119

120

121

122

123

124

125

126

127

128

129

130

131

132

133

134

135

136

137

138

139

140

141

142

143

144

145

146

147

148

149

150

151

152

153

154

155

156

157

158

159

160

161

162

163

164

165

166

167

168

169

170

171

172

173

174

175

176

177

178

179

180

181

182

183

184

185

186

187

188

189

190

191

192

193

194

195

196

197

198

199

200

GenBank version 4.5
Copyright 1998 Computer Ltd

ON Protein: Protein Search using SW Model

File: 09-030-061-1 Search time: 93.17 seconds
(without alignments)

3.980 Million cell updates/sec

Header:

US-09-030-061-1

Sequence:

1 NC001616

Scoring table:

PROGMM62

Search: 100763 seqs, 55169189 residues

Database:

SPRMBL_8.*
1: SP_Fungi.*
2: SP_Human.*
3: SP_Invertebrate.*
4: SP_Mammal.*
5: SP_Mhc.*
6: SP_Organeller.*
7: SP_Phage.*
8: SP_Plant.*
9: SP_Protozoa.*
10: SP_Rodent.*
11: SP_Virus.*
12: SP_Xenobiotic.*
13: SP_Unclassified.*
14: SP_Xenoc.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	FR	ID	Description
1	31	100.0	194	2	075599 homo sapien
2	31	100.0	194	9	098749 rat/rus nrr
3	28	90.3	782	10	P76808 esch-rilicla
4	28	90.3	110	11	057532 vaccinia v
5	28	90.3	117	11	056217 camelpox v
6	28	90.3	110	11	056272 cowpox v
7	28	90.3	110	11	083542 mousepox v
8	28	90.3	110	11	090188 monkeypox v
9	28	90.3	548	14	058508 methanococ
10	28	87.1	126	3	001641 drosophila
11	27	87.1	426	3	062531 drosophila
12	27	87.1	42	3	025522 manduca sex
13	27	87.1	395	3	025495 manduca sex
14	27	87.1	426	3	002382 caenorhabd
15	27	87.1	1763	3	017901 caenorhabd
16	27	87.1	1763	3	017901 caenorhabd
17	27	87.1	1763	3	017901 caenorhabd
18	27	87.1	216	9	P96535 helicobacte
19	27	87.1	539	9	P74814 spirochaete
20	27	87.1	539	9	P74814 spirochaete
21	27	87.1	539	9	P74814 spirochaete
22	27	87.1	539	9	P74814 spirochaete
23	27	87.1	539	9	P74814 spirochaete
24	27	87.1	539	9	P74814 spirochaete
25	27	87.1	539	9	P74814 spirochaete
26	27	87.1	539	9	P74814 spirochaete
27	27	87.1	539	9	P74814 spirochaete
28	27	87.1	539	9	P74814 spirochaete
29	27	87.1	539	9	P74814 spirochaete
30	27	87.1	539	9	P74814 spirochaete

ALIGNMENTS

RESULT	ID	Score	Query Match	Best Local Similarity	100.00	Pred. No. 4.3	Misaligns	0	Indels	0	Gaps
1	075599	PRELIMINARY	PRI	194 AA							
2	098749	PRELIMINARY	PRI	194 AA							
3	075599	PRELIMINARY	PRI	194 AA							
4	01-NOV-1998	08	LAST SEQUENCE UPDATE								
5	01-NOV-1998	08	LAST SEQUENCE UPDATE								
6	01-NOV-1998	08	LAST SEQUENCE UPDATE								
7	01-NOV-1998	08	LAST SEQUENCE UPDATE								
8	01-NOV-1998	08	LAST SEQUENCE UPDATE								
9	01-NOV-1998	08	LAST SEQUENCE UPDATE								
10	01-NOV-1998	08	LAST SEQUENCE UPDATE								
11	01-NOV-1998	08	LAST SEQUENCE UPDATE								
12	01-NOV-1998	08	LAST SEQUENCE UPDATE								
13	01-NOV-1998	08	LAST SEQUENCE UPDATE								
14	01-NOV-1998	08	LAST SEQUENCE UPDATE								
15	01-NOV-1998	08	LAST SEQUENCE UPDATE								
16	01-NOV-1998	08	LAST SEQUENCE UPDATE								
17	01-NOV-1998	08	LAST SEQUENCE UPDATE								
18	01-NOV-1998	08	LAST SEQUENCE UPDATE								
19	01-NOV-1998	08	LAST SEQUENCE UPDATE								
20	01-NOV-1998	08	LAST SEQUENCE UPDATE								
21	01-NOV-1998	08	LAST SEQUENCE UPDATE								
22	01-NOV-1998	08	LAST SEQUENCE UPDATE								
23	01-NOV-1998	08	LAST SEQUENCE UPDATE								
24	01-NOV-1998	08	LAST SEQUENCE UPDATE								
25	01-NOV-1998	08	LAST SEQUENCE UPDATE								
26	01-NOV-1998	08	LAST SEQUENCE UPDATE								
27	01-NOV-1998	08	LAST SEQUENCE UPDATE								
28	01-NOV-1998	08	LAST SEQUENCE UPDATE								
29	01-NOV-1998	08	LAST SEQUENCE UPDATE								
30	01-NOV-1998	08	LAST SEQUENCE UPDATE								

[illegible]

Q83542	PRELIMINARY;	PRT;	110 AA
ID	Q83542		


```

RN      [1]
RP      SEQUENCE FROM N.A.
EX      MEDLINE: 97067009.
FA      JIANG H., WANG Y., HEWANG Y., MULNIX A.B., KADH J., MOLE K.,
FA      KANDU M.P.:
RT      "Organization of serpin gene1 from Manduca sexta. Evolution of a
RT      family of alternate exons encoding the reactive site loop."
RL      1. BIOL. CHIM. 271:28017-28023(1996).
DR      EMBL: 0563851; 01378131.
DR      PIRAM: PF00079; Serpin1.1.
DR      2.
DR      3.
DR      4.
DR      5.
DR      6.
DR      7.
DR      8.
DR      9.
DR      10.
DR      11.
DR      12.
DR      13.
DR      14.
DR      15.
DR      16.
DR      17.
DR      18.
DR      19.
DR      20.
DR      21.
DR      22.
DR      23.
DR      24.
DR      25.
DR      26.
DR      27.
DR      28.
DR      29.
DR      30.
DR      31.
DR      32.
DR      33.
DR      34.
DR      35.
DR      36.
DR      37.
DR      38.
DR      39.
DR      40.
DR      41.
DR      42.
DR      43.
DR      44.
DR      45.
DR      46.
DR      47.
DR      48.
DR      49.
DR      50.
DR      51.
DR      52.
DR      53.
DR      54.
DR      55.
DR      56.
DR      57.
DR      58.
DR      59.
DR      60.
DR      61.
DR      62.
DR      63.
DR      64.
DR      65.
DR      66.
DR      67.
DR      68.
DR      69.
DR      70.
DR      71.
DR      72.
DR      73.
DR      74.
DR      75.
DR      76.
DR      77.
DR      78.
DR      79.
DR      80.
DR      81.
DR      82.
DR      83.
DR      84.
DR      85.
DR      86.
DR      87.
DR      88.
DR      89.
DR      90.
DR      91.
DR      92.
DR      93.
DR      94.
DR      95.
DR      96.
DR      97.
DR      98.
DR      99.
DR      100.
DR      101.
DR      102.
DR      103.
DR      104.
DR      105.
DR      106.
DR      107.
DR      108.
DR      109.
DR      110.
DR      111.
DR      112.
DR      113.
DR      114.
DR      115.
DR      116.
DR      117.
DR      118.
DR      119.
DR      120.
DR      121.
DR      122.
DR      123.
DR      124.
DR      125.
DR      126.
DR      127.
DR      128.
DR      129.
DR      130.
DR      131.
DR      132.
DR      133.
DR      134.
DR      135.
DR      136.
DR      137.
DR      138.
DR      139.
DR      140.
DR      141.
DR      142.
DR      143.
DR      144.
DR      145.
DR      146.
DR      147.
DR      148.
DR      149.
DR      150.
DR      151.
DR      152.
DR      153.
DR      154.
DR      155.
DR      156.
DR      157.
DR      158.
DR      159.
DR      160.
DR      161.
DR      162.
DR      163.
DR      164.
DR      165.
DR      166.
DR      167.
DR      168.
DR      169.
DR      170.
DR      171.
DR      172.
DR      173.
DR      174.
DR      175.
DR      176.
DR      177.
DR      178.
DR      179.
DR      180.
DR      181.
DR      182.
DR      183.
DR      184.
DR      185.
DR      186.
DR      187.
DR      188.
DR      189.
DR      190.
DR      191.
DR      192.
DR      193.
DR      194.
DR      195.
DR      196.
DR      197.
DR      198.
DR      199.
DR      200.
DR      201.
DR      202.
DR      203.
DR      204.
DR      205.
DR      206.
DR      207.
DR      208.
DR      209.
DR      210.
DR      211.
DR      212.
DR      213.
DR      214.
DR      215.
DR      216.
DR      217.
DR      218.
DR      219.
DR      220.
DR      221.
DR      222.
DR      223.
DR      224.
DR      225.
DR      226.
DR      227.
DR      228.
DR      229.
DR      230.
DR      231.
DR      232.
DR      233.
DR      234.
DR      235.
DR      236.
DR      237.
DR      238.
DR      239.
DR      240.
DR      241.
DR      242.
DR      243.
DR      244.
DR      245.
DR      246.
DR      247.
DR      248.
DR      249.
DR      250.
DR      251.
DR      252.
DR      253.
DR      254.
DR      255.
DR      256.
DR      257.
DR      258.
DR      259.
DR      260.
DR      261.
DR      262.
DR      263.
DR      264.
DR      265.
DR      266.
DR      267.
DR      268.
DR      269.
DR      270.
DR      271.
DR      272.
DR      273.
DR      274.
DR      275.
DR      276.
DR      277.
DR      278.
DR      279.
DR      280.
DR      281.
DR      282.
DR      283.
DR      284.
DR      285.
DR      286.
DR      287.
DR      288.
DR      289.
DR      290.
DR      291.
DR      292.
DR      293.
DR      294.
DR      295.
DR      296.
DR      297.
DR      298.
DR      299.
DR      300.
DR      301.
DR      302.
DR      303.
DR      304.
DR      305.
DR      306.
DR      307.
DR      308.
DR      309.
DR      310.
DR      311.
DR      312.
DR      313.
DR      314.
DR      315.
DR      316.
DR      317.
DR      318.
DR      319.
DR      320.
DR      321.
DR      322.
DR      323.
DR      324.
DR      325.
DR      326.
DR      327.
DR      328.
DR      329.
DR      330.
DR      331.
DR      332.
DR      333.
DR      334.
DR      335.
DR      336.
DR      337.
DR      338.
DR      339.
DR      340.
DR      341.
DR      342.
DR      343.
DR      344.
DR      345.
DR      346.
DR      347.
DR      348.
DR      349.
DR      350.
DR      351.
DR      352.
DR      353.
DR      354.
DR      355.
DR      356.
DR      357.
DR      358.
DR      359.
DR      360.
DR      361.
DR      362.
DR      363.
DR      364.
DR      365.
DR      366.
DR      367.
DR      368.
DR      369.
DR      370.
DR      371.
DR      372.
DR      373.
DR      374.
DR      375.
DR      376.
DR      377.
DR      378.
DR      379.
DR      380.
DR      381.
DR      382.
DR      383.
DR      384.
DR      385.
DR      386.
DR      387.
DR      388.
DR      389.
DR      390.
DR      391.
DR      392.
DR      393.
DR      394.
DR      395.
DR      396.
DR      397.
DR      398.
DR      399.
DR      400.
DR      401.
DR      402.
DR      403.
DR      404.
DR      405.
DR      406.
DR      407.
DR      408.
DR      409.
DR      410.
DR      411.
DR      412.
DR      413.
DR      414.
DR      415.
DR      416.
DR      417.
DR      418.
DR      419.
DR      420.
DR      421.
DR      422.
DR      423.
DR      424.
DR      425.
DR      426.
DR      427.
DR      428.
DR      429.
DR      430.
DR      431.
DR      432.
DR      433.
DR      434.
DR      435.
DR      436.
DR      437.
DR      438.
DR      439.
DR      440.
DR      441.
DR      442.
DR      443.
DR      444.
DR      445.
DR      446.
DR      447.
DR      448.
DR      449.
DR      450.
DR      451.
DR      452.
DR      453.
DR      454.
DR      455.
DR      456.
DR      457.
DR      458.
DR      459.
DR      460.
DR      461.
DR      462.
DR      463.
DR      464.
DR      465.
DR      466.
DR      467.
DR      468.
DR      469.
DR      470.
DR      471.
DR      472.
DR      473.
DR      474.
DR      475.
DR      476.
DR      477.
DR      478.
DR      479.
DR      480.
DR      481.
DR      482.
DR      483.
DR      484.
DR      485.
DR      486.
DR      487.
DR      488.
DR      489.
DR      490.
DR      491.
DR      492.
DR      493.
DR      494.
DR      495.
DR      496.
DR      497.
DR      498.
DR      499.
DR      500.
DR      501.
DR      502.
DR      503.
```


DI 01-NOV-1998 (HEMELBEL, 08, LAST ANNOTATION UPDATE)
 DE C10C5.6 PROTEIN.
 GN C10C5.6
 OS CAENORHABDITIS ELEGANS.
 OC EMBRYONAL DEVELOPMENT, NEMATODA, SECERNENTEA, RHABDITIA, RHABDITIDA,
 OC RHABDITINA, RHABDITIDAE, RHABDITINAE, PTEROPHYTES, CAENORHABDITIS.
 RN 11
 RP SEQUENCE FROM N.A.
 RA MATTHEWS P.
 RL SUBMITTED (NOV-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN 12
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 94150718.
 RA WILSON P., AINSWORTH P., ANDERSON K., BAYNES C., BERKS M., BONFIELD J.,
 RA BERTON T., CONNELL M., GOSSET I., GUMPER J., JOHNSON A., GRAYSON M.,
 RA DEAR S., GUNZ L., EMERIN P., FAVELLO A., FULTON L., GARDNER A., GREEN P.,
 RA HAWKINS T., HILFERT L., JEFF M., JOHNSON L., JONES M., KERSHAW J.,
 RA KRISTEN T., LAISTER N., LAURENCE P., LIGHTNING J., LLOYD C.,
 RA MCMURRAY A., MORTIMORE B., O'CALLAGHAN M., PARSONS J., PERCY C.,
 RA RIFKIN L., POOPRA A., SAUNDERS D., SHOWNKEEN R., SMALDON N., SMITH A.,
 RA SONNEMMER E., STADEN P., STELSON J., THIERRY-MIEG J., THOMAS K.,
 RA VAUGHAN M., VANHAN K., WATERSTON R., WATSON A., WEINSTOCK C.,
 RA WILKINSON-SPOAT J., WOLDMAN P.,
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans."
 RL NATURE 368:32-38(1994).
 DR EMBL: 258214; E1301758;
 DR EMBL: 259052; E1301758; JOINED.
 DR EMBL: 259462; E1302535;
 DR EMBL: 258214; E1302535; JOINED.
 SO SEQUENCE 1763 AA; 201972 MW; FEDA34C5 CFC32;

Query Match 87.18; Score 27; DB 3; Length 1763;
 Best Local Similarity 83.38; Fred. No. 4.1e-02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NDOVLF 5
 11111
 Db 183 NDRYLF 188

Search completed: June 22, 1999, 11:01:19
 Job time: 165 sec

100

101

102

103

104

105

106

107

108

109

110

111

112

113

114

115

116

117

118

119

120

121

122

123

124

125

126

127

128

129

130

131

132

133

134

135

136

137

138

139

140

141

142

143

144

145

146

147

148

149

150

151

152

153

154

155

156

157

158

159

160

161

162

163

164

165

166

167

168

169

170

171

172

173

174

175

176

177

178

179

180

181

182

183

184

185

186

187

188

189

190

191

192

193

194

195

196

197

198

199

200

01 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 02 INTERLEUKIN-18 PROMOTOR (IL-18) (INTERFERON-GAMMA INDUCING FACTOR)
 03 (H18-GAMMA-INDUCING FACTOR) (INTERLEUKIN 1 GAMMA) (IL-1 GAMMA)
 04 IL18 OR IGIF
 05 RATTUS NORVEGICUS (RAT)
 06 E. KAKABUTA, METAZA, CHOEATA, VERTEBRATA, THALAZOA, MAMMALIA
 07 EUTHERIA, RODENTIA,
 08 [1]
 09 SEQUENCE FROM N.A.
 10 STRAIN=SEPAGE-DRALEY; TISSUE=ADIPENAL GLAND;
 11 MEDLINE# 97152963.
 12 CONTI B., JAHNG J.W., TINTI C., SON J.H., JOH F.H.,
 13 J. BIOL. CHEM. 272(26):2037(1997).
 14 -1- FOUNDED: AGREENTS NATIONAL KILLER CELL ACTIVITY IN SPLEN CELLS
 15 AND STIMULATES INTERFERON GAMMA PRODUCTION IN 1 HELPER TYPE 1
 16 CELLS.
 17 EMBL: 0777776; G1809129; -;
 18 EMBL: 0777777; G1809131; -;
 19 CYTOKINE; ALTERNATIVE SPLICING;
 20 PROPEP 1 36 BY SIMILARITY.
 21 CHAIN 37 INTERLEUKIN-18
 22 VARSPLIC 121 139 MISSING (IN ISOFORM ALPHA).
 23 SEQUENCE 194 AA; 23570 MW; 4974217 MD; 320

```

Query Match 100.0% Score 31; DB 1; Length 194;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 5; Conservative 0; Mismatches 0; Gaps 0

CY 1 NDQVLF 6
      |||||
DB 52 NDQVLF 57

RESULT 5
ICN2_LACLA
ICN2_LACLA STANDARD 451 552 AA.
AC P43609;
DT 01-OCT-1994 (PREL. 30, CREATED)
DI 01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
DI 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
EA LACTALIN 485; LACTOGENOIN BIOSYNTHESIS PROTEIN ENDR2.
GN ENDR2.
OS LACTOGENOIN LACTIS (GENUS: LACTIS) (SILPOTOMYXUS LACTIS).
OC PROKARYOTA; FIRMICUTES; CLOIDI; SIPIREPOTOCACEAE.
RN [1]
F1 SEQUENCE FROM N.A.
F2 STRAIN=ADRIA 951030;
RX MEDLINE: 94398641.
RA PINTO A., TRFOP R., LE FROM S., IMVALLI E., B. BROSCHI G.M.,
  PENNED J.P.;
RL APPL. ENVIRON. MICROBIOL. 60:1652-1657(1994);
  -1- FUNCTION: COULD BE IMPLICATED IN THE PROTECTING OF THE EXP. RT
  PROCESSES OF THE LACTIOTIC LACTISIN 485/LACTOGENOIN DR.
DR EMBL: U04057: G433322; .
SV SEQUENCE 522 AA; 111008 MW; 5541418 MDCC27.

Query Match 96.8% Score 30; DB 1; Length 922;
Best Local Similarity 83.3%; Pred. No. 15;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0

CY 1 NDQVLF 6
      |||||
DB 569 NDQVLF 574

RESULT 6
YOGG_HAEIN
YOGG_HAEIN STANDARD; PRT: 186 AA.
AC P43980;
DT 01-NOV-1995 (REL. 32, CREATED)

```

FT	SIGNAL	1	42	POTENTIAL.
FT	CHAIN	43	769	INTERIN. BETA-8.
FT	DOMAIN	44	684	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	685	704	POTENTIAL.
FT	DOMAIN	705	759	CYCLOLASMIC (POTENTIAL).
FT	DOMAIN	471	429	Cysteine-RICH REPEATS.
FT	REPEAT	471	510	1.
FT	REPEAT	511	552	11.
FT	REPEAT	553	592	11.
FT	REPEAT	592	639	IV.
FT	CARBOHYD	639	723	POTENTIAL.
FT	CARBOHYD	402	432	POTENTIAL.
FT	CARBOHYD	431	441	POTENTIAL.
FT	CARBOHYD	431	431	POTENTIAL.
FT	CARBOHYD	456	456	POTENTIAL.
FT	CARBOHYD	456	456	POTENTIAL.
FT	CARBOHYD	648	648	POTENTIAL.
SEQUENCE		709 AA:	85931 MW:	A3915040 CRC32:

Quality Match	Post Local Similarity	Score	DB	Length
Matches	5, Conserved	92.3%	1.	100
			Mismatches	0, Indels
				Gaps

```

RESULT 8
MPOC_MVGC ID MPOC_MVGC STANDARD: perl 1052 AA
A: F-777, 047491, 047498, 04754, 04755, 04757;
GT 01-AUG-1991 (PEL: 19, CREATED)
DT 01-AUG-1991 (PEL: 19, LAST SEQUENCE UPDATED)
DT 01-NOV-1997 (PEL: 35, LAST ANNOTATION UPDATE)
CN MPOC PROTEIN PRECURSOR.
GN MGPC OR MG192.
OS MYCOPLASMA GENITALIUM.
OC PRAKARYOTA: TEMPERATES: MOLLUSCS: MYCOPLASMA: MYCOPLASMATALES:
OC MYCOPLASMACEAE.
11)
SEQUENCE FROM N.A.
STRAIN:MG192 11112 / G-377
MEDLINE: 90060915.
RA INAMINE J.M., LOCHEL S., COLLIER A.M., BARILE M.F., HU P.-C.:
GENE 92,359,267(1989).
PI 12)
SEQUENCE FROM N.A.
STRAIN:MG192 11112 / G-377
MEDLINE: 94026345.
RA FRAGER J.M., GOTTARLT D., WHITE G., ADAMS M.D., CLAYTON R.A.,
FRITZCHMAN J.L., HOLT J.T., KERRIDGE A.P., SHYEN G., KELLEY J.M.,
WILKINSON J.L., WEIDMAN J.P., SMALL K.V., SANDERS M., FUHRMANN J.L.,
NIVEN T.T., UTTERLEY P., SAYER E.M., PHILLIPS G.A., MERRICK J.M.,
TOMRAT T.F., THORBERY P.A., BOTT K.F., HU P.-C., LIGIER T.S.,
FERGUSON S.M., SMITH H.B., HUTCHISON C.A. III, VENTER 1992.
SCIENT 920337,433(1992).
13)
SEQUENCE OF 50-1271, 200370, 441112 AND 364-1052.
STRAIN:MG192 11112 / G-377
MEDLINE: 94075930.
RA PETERSON S.N., HU P.-C., BOTT K.F., HUTCHISON C.A. III;
PI BACTERIOL. 175(7918-7930(1993)).
14)
SEQUENCE OF 759-954 FROM N.A.
STRAIN:MG192 11112 / G-377
MEDLINE: 92051396.
RA PETERSON S.N., SCHRAM M., HU P.-C., BOTT K.F., HUTCHISON C.A. III;
NCBI:G1502607-
EMBL: M14317 G1502607-
FBI: 047491, 047498, 04754, 04755, 04757.
EMBL 905124; G409890; -

```


1 0927 A. ...
 2 AN ...
 3 ...
 4 ...
 5 ...
 6 ...
 7 ...
 8 ...
 9 ...
 10 ...
 11 ...
 12 ...
 13 ...
 14 ...
 15 ...
 16 ...
 17 ...
 18 ...
 19 ...
 20 ...
 21 ...
 22 ...
 23 ...
 24 ...
 25 ...
 26 ...
 27 ...
 28 ...
 29 ...
 30 ...
 31 ...
 32 ...
 33 ...
 34 ...
 35 ...
 36 ...
 37 ...
 38 ...
 39 ...
 40 ...
 41 ...
 42 ...
 43 ...
 44 ...
 45 ...
 46 ...
 47 ...
 48 ...
 49 ...
 50 ...

Query Match 100.0% Score 33: DB 1: Length 157;
 Best Local Similarity 100.0% Pred. No. 2.7;
 Matches 6: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 1 FEDMTD 6
 2 ...
 3 ...
 4 ...
 5 ...
 6 ...
 7 ...
 8 ...
 9 ...
 10 ...
 11 ...
 12 ...
 13 ...
 14 ...
 15 ...
 16 ...
 17 ...
 18 ...
 19 ...
 20 ...
 21 ...
 22 ...
 23 ...
 24 ...
 25 ...
 26 ...
 27 ...
 28 ...
 29 ...
 30 ...
 31 ...
 32 ...
 33 ...
 34 ...
 35 ...
 36 ...
 37 ...
 38 ...
 39 ...
 40 ...
 41 ...
 42 ...
 43 ...
 44 ...
 45 ...
 46 ...
 47 ...
 48 ...
 49 ...
 50 ...

CC PCR amplification of the cDNA (see also T12406-10) and expression
 CC in Escherichia coli XL-1 blue MRFkan allowed production of recombinant
 CC inducer protein. This was used to convert lymphoma u-1 cells
 CC produced anti IFN-gamma inducer protein monoclonal antibody H-1mAb.
 CC useful in the detection and purification of the inducer protein
 CC (see also R99558).
 SU Sequence 157 AA:

Query Match 100.0% Score 33: DB 1: Length 157;
 Best Local Similarity 100.0% Pred. No. 2.7;
 Matches 6: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 1 FEDMTD 6
 2 ...
 3 ...
 4 ...
 5 ...
 6 ...
 7 ...
 8 ...
 9 ...
 10 ...
 11 ...
 12 ...
 13 ...
 14 ...
 15 ...
 16 ...
 17 ...
 18 ...
 19 ...
 20 ...
 21 ...
 22 ...
 23 ...
 24 ...
 25 ...
 26 ...
 27 ...
 28 ...
 29 ...
 30 ...
 31 ...
 32 ...
 33 ...
 34 ...
 35 ...

RESULT 4
 ID R99558 standard: Protein: 157 AA.
 AC R99558:
 DT 28-SEP-1996 (first entry)
 DE Human mature interferon-gamma inducer protein.
 KW Interferon-gamma inducer protein; IFN-gamma; antiviral; virocid;
 KW antitumor; antibacterial; immunoregulator; adoptive immunotherapy;
 KW therapy; cancer.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT misc_difference 73
 FT ...
 PN BP-712931-A2.
 PD 22-MAY-1996.
 PE 16-NOV-1995: 408955.
 PR 15-NOV-1994: JP-304203.
 PR 23-FEB-1995: JP-058240.
 PR 10-MAR-1995: JP-078357.
 PR 18-SEP-1995: JP-262082.
 PR 29-SEP-1995: JP-274988.
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 PI Fukuda S, Kohno K, Kunitaga T, Furimaga M, Okamura H,
 PI Tanouchi M, Tanimoto T, Toriige K, Ushio S;
 DB N-PSDB: T32402.
 DR DNA encoding interferon-gamma protein, inducing polypeptide - useful
 PT to treat and prevent, e.g. viral disease, malignancies and immune
 PT disorders
 PS Claim 1: Page 40: 48pp: English.
 CC A novel human protein (R99558) induces interferon-gamma (IFN-gamma)
 CC protein by immunocompetent cells. It enhances the cytotoxicity of
 CC killer cells and/or induces the formation of killer cells (e.g.,
 CC NK cells, lymphokine-activated killer (LAK) cells, and cytotoxic
 CC T-cells). Recombinant IFN-gamma inducer protein can be produced in
 CC high yields using host cells, esp. Escherichia coli, transformed
 CC with a vector carrying the encoding cDNA (T32402). It is useful
 CC as an antiviral, antitumor, antibacterial, immunoregulatory and
 CC blood platelet enhancing agent, and can be used in adoptive
 CC immunotherapy. It is also used to raise monoclonal antibodies.
 CC A full length sequence is given in R99550.
 SO Sequence 157 AA:

Query Match 100.0% Score 33: DB 1: Length 157;
 Best Local Similarity 100.0% Pred. No. 2.7;
 Matches 6: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 1 FEDMTD 6
 2 ...
 3 ...
 4 ...
 5 ...
 6 ...
 7 ...
 8 ...
 9 ...
 10 ...
 11 ...
 12 ...
 13 ...
 14 ...
 15 ...
 16 ...
 17 ...
 18 ...
 19 ...
 20 ...
 21 ...
 22 ...
 23 ...
 24 ...
 25 ...
 26 ...
 27 ...
 28 ...
 29 ...
 30 ...
 31 ...
 32 ...
 33 ...
 34 ...
 35 ...

ID R99559 standard. Protein. 157 AA.
 AC R99559.
 DT 29-SEP-1996 (first entry)
 DE Mouse gamma interferon gamma inducer protein.
 KW Interferon gamma inducer protein, IFN-gamma, activator, cytokine,
 K1 anti-tumor, antitubercular, immunoregulator, adoptive immunotherapy,
 KM choroid plexus.
 OS Mus sp.
 PE 22-MAY-1996.
 PR 10-NOV-1995: J08055.
 PR 15-NOV-1994: JP-304203.
 PR 22-FEB-1995: JP-080340.
 PR 10-MAR-1995: JP-078357.
 PR 18-SEP-1995: JP-262062.
 PR 23-SEP-1995: JP-274988.
 PA (HAYAB) HAYASHIBARA SEIBUTSU KAGAKU.
 PI Furuda S, Kohno K, Kunitada T, Torigoe K, Ushio S.
 DR Taniguchi M, Taniguchi T, Torigoe K, Ushio S.
 DR N-PSDB: 132403.
 DT 29-SEP-1996 (first entry)
 DE DNA encoding interferon gamma protein-inducing polypeptide - useful
 PI to treat and prevent, e.g. viral disease, malignancies and immune
 PT disorders.
 PS Example A-3-2: Page 36-37, 48ff. English.
 CC A novel mouse protein (R99559) induces interferon-gamma (IFN-gamma)
 CC protein by immunocompetent cells. Its sequence was deduced from
 CC that of a cDNA clone (132403) isolated from a mouse liver library.
 CC Functional IFN-gamma inducer protein can be produced in high yields
 CC using host cells, esp. Escherichia coli, transformed with a vector
 CC carrying the cDNA.
 CC Sequence 167 AA.
 SQ Sequence 167 AA.
 Query Match 100.0% Score 33 DB 1 Length 157
 Best local similarity 100.0% Prod. No. 2.7
 Matches 6 Conservative 0 Mismatches 0 Indels 0 Gaps 0
 DB 29 FEBMD 14
 QY 1 FEBMD 6
 ID R99560 standard. Protein. 193 AA.
 AC R99560.
 DT 29-SEP-1996 (first entry)
 DE Human interferon gamma inducer protein.
 KW Interferon gamma inducer protein, IFN-gamma, activator, cytokine,
 KM anti-tumor, antitubercular, immunoregulator, adoptive immunotherapy,
 KM choroid plexus.
 OS Homo sapiens.
 PE 22-MAY-1996.
 PR 10-NOV-1995: J08055.
 PR 15-NOV-1994: JP-304203.
 PR 22-FEB-1995: JP-080340.
 PR 10-MAR-1995: JP-078357.
 PR 18-SEP-1995: JP-262062.
 PR 24-SEP-1995: JP-274989.
 PA (HAYAB) HAYASHIBARA SEIBUTSU KAGAKU.
 PI Furuda S, Kohno K, Kunitada T, Kunitada M, Okamura H.
 DR Taniguchi M, Taniguchi T, Torigoe K, Ushio S.
 DR N-PSDB: 132404.
 DT 29-SEP-1996 (first entry)
 DE DNA encoding interferon gamma protein-inducing polypeptide - useful
 PI to treat and prevent, e.g. viral disease, malignancies and immune
 PT disorders.
 PS Claim 6: Page 41-42, 48pp. English.
 CC The major portion of a novel human protein (R99560) induces
 CC interferon gamma (IFN-gamma) protein by immunocompetent cells. It
 CC is the product of a cDNA clone (132404) obtained from a human liver
 CC library. The protein enhances the cytotoxicity of killer cells
 CC and/or induces the formation of killer cells (e.g. NK cells).
 CC Lymphokine-activated killer (LAK) cells, and cytotoxic T-cells,
 CC The mouse protein (see also R99559) is useful as an antiviral,
 CC anti-tumor, antitubercular, immunoregulatory and blood platelet
 CC inducing agent, and can be used to develop immunoreactivity. It is
 CC also used to raise monoclonal antibodies.
 CC Sequence 193 AA.
 SQ Sequence 193 AA.
 Query Match 100.0% Score 33 DB 1 Length 18
 Best local similarity 100.0% Prod. No. 1.1
 Matches 4 Conservative 0 Mismatches 0 Indels 0 Gaps 0
 DB 4 FEBMD 9
 QY 1 FEBMD 6
 ID R99562 standard. Peptide. 18 AA.
 AC R99562.
 DT 29-SEP-1996 (first entry)
 DE Interferon gamma inducer protein (IFN-gamma) activator, cytokine,
 KW anti-tumor, antitubercular, immunoregulator, adoptive immunotherapy,
 KM therapy, cancer.
 OS Mus sp.
 PE 22-MAY-1996.
 PR 10-NOV-1995: J08055.
 PR 15-NOV-1994: JP-304203.
 PR 23-FEB-1995: JP-080340.
 PR 10-MAR-1995: JP-078357.
 PR 18-SEP-1995: JP-262062.
 PR 29-SEP-1995: JP-274988.
 PA (HAYAB) HAYASHIBARA SEIBUTSU KAGAKU.
 PI Furuda S, Kohno K, Kunitada T, Kunitada M, Okamura H.
 PI Taniguchi M, Taniguchi T, Torigoe K, Ushio S.
 DR Taniguchi M, Taniguchi T, Torigoe K, Ushio S.
 DR N-PSDB: 132405.
 DT 29-SEP-1996 (first entry)
 DE DNA encoding interferon gamma protein-inducing polypeptide - useful
 PI to treat and prevent, e.g. viral disease, malignancies and immune
 PT disorders.
 PS Example A-3-6: Page 37, 48pp. English.
 CC Triptic peptides (R99561 and R99562) correspond to amino acids
 CC 29-10-33-43, respectively, of a novel interferon-gamma
 CC (IFN-gamma) inducer protein identified in mouse liver. The
 CC peptide's amino acid sequence, PFF FFFRS (73245-66) that were
 CC utilized in the amplification of mouse liver cDNA, leading to
 CC the isolation of a clone (132405) coding for mouse IFN-gamma
 CC inducer protein (R99559).
 CC Sequence 18 AA.
 SQ Sequence 18 AA.

[illegible]

```

Cv      1 FEDMTD 6
        |||||
Db      4 FEDMTD 9

RESULT 10
W24258 standard. Protein: 157 AA.
AC      W24258: 15-OCT-1997 (first entry)
DE      Human protein for induction of interferon-gamma.
KW      Interferon-gamma; immunocompetent cell; malignant tumour;
OS      viral disease; bacterial infection; immune disease.
FH      Key
FT      MISC_difference 73
        /note= "Encoded by AYI"
FN      J0157180-A.
PD      17-JUN-1997.
PE      24-JAN-1995: 028722.
PK      04-OCT-1995: JP-278906.
PR      10-MAR-1995: JP-078357.
PS      29-SEP-1995: JP-274988.
PA      (HAYB.) HAYASHIBARA SEIMUSU KAGAKU.
PE      WPI: 97-269391/74.
LR      N-PSDB: 180209.
PT      A drug containing a polypeptide which induces interferon-gamma
PT      useful for treating e.g. malignant tumours, viral, bacterial or
PT      immune diseases.
PS      Claim 1: Page 9; 12pp; Japanese.
CC      This sequence represents a protein which induces interferon-gamma
CC      production in immunocompetent cells. This protein may be used as
CC      the major component in a drug for the prevention and treatment of
CC      e.g. malignant tumours, viral diseases, bacterial infections and
CC      immune diseases.
SQ      Sequence 157 AA:

Query Match      100.0%; Score 33; DB 1; Length 157;
Best Local Similarity 100.0%; Prod. No. 2.7;
Matches      6; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Cv      1 FEDMTD 6
        |||||
Db      30 FEDMTD 35

RESULT 11
W31757 standard. Protein: 193 AA.
AC      W31757: 15-JAN-1998 (first entry)
DE      Interferon gamma inducing factor-2 (IGIF-2) P140 variant.
KW      Interferon-gamma; inducing factor-2; IGIF-2; interferon-gamma; human
KW      inflammation; proliferation; differentiation; maturation; tissue damage.
OS      Homo sapiens.
FH      Key
FT      MISC_difference 140
        /label= P1401
        /note= "Wild type Arg is replaced by Ile"
FN      W09724441-A1.
PD      10-JUL-1997.
PE      28-DEC-1995: 070432.
PR      29-DEC-1995: US-580667.
PA      (IMCY-) IMCYIE PHARM INC.
PK      Cocks BG, Coleman P, Hawkins PR.
PE      WPI: 97-363677/33.
LR      N-PSDB: T74988.
PT      Novel interferon gamma inducing factor-2, used to screen for
PT      compounds to diagnose, treat or prevent tissue damage associated

```

PT With inflammation
PS Claim 3: Page 7: 50pp: English.
CC This protein sequence represents an interferon gamma inducing factor-2 (IGIF-2) variant, identified from a liver cDNA library. This sequence differs from IGIF-2 identified from a T-lymphocyte cDNA library (W22047), in that amino acid 140 is found to be changed from Arg to Ile. A second variant, W22049, also exists. Probes derived from the nucleic acid sequence may be used to quantify the expression of IGIF-2 in conditions that are associated with inflammation or aberrant expression of IGIF-2. The protein can be used to screen for compounds that interact with IGIF-2, such as inhibitors of other inhibitors (especially ribozymes or antisense sequences) of IGIF-2 expression or activity. The protein can also be used to diagnose, prevent or treat IGIF-2 induction or proliferation, differentiation or maturation of leucocytes or lymphocytes, especially in relation to tissue damage associated with inflammation.
CC IGIF-2 is a protein that has not appear in the specification. It has been used to identify the IGIF-2 sequence presented in W22047.
SQ Sequence 133 AA:

Query Match 100.0% Score 33 DB 1 Length 193
Best Local Similarity 100.0% Prod. No. 3.4
Matches 6: Conservative 0: Mismatches 0: Indels 0: Gaps 0

QY 1 FEDMD 6
DB 56 FEDMD 71

RESULT 13
W22047 W22047 standard, peptide, 137 AA.
ID W22047
AC W22047
DE 14-JAN-1998 (first entry)
DE Interferon gamma inducing factor-2 (IGIF-2) protein.
KW Interferon gamma inducing factor-2, IGIF-2, leucocyte, lymphocyte, inflammation, proliferation, differentiation, maturation, tissue damage, human.
OS Homo sapiens.
PN W0972441-A1.
PD 10-SEP-1997.
PF 20-SEP-1996: JP-269105.
PR 26-SEP-1996: JP-270725.
PA (HVA) INOYE PHARM, INC.
PI Cocke R, Coleman P, Hawkins P.
DR WPI: 97-363677/33.
DR N-PSDB: 774987.
PT Novel interferon gamma inducing factor-2 - used to screen for compounds to diagnose, treat or prevent tissue damage associated with inflammation.
PS Claim 1: Page 40: 50pp: English.
CC This is the protein sequence of interferon gamma inducing factor-2 (IGIF-2). An IGIF-2 variant (W22049) and an IGIF variant (W22049), which may be an alternate transcript, also exist. Probes derived from the nucleic acid sequence can be used to quantify the expression of IGIF-2 in conditions that are associated with inflammation or aberrant expression of IGIF-2. The protein can be used to screen for compounds that interact with IGIF-2, such as antibodies, antagonists or other inhibitors (especially ribozymes or antisense sequences) of IGIF-2 expression or activity. The protein can also be used to diagnose, prevent or treat IGIF-2 induction or proliferation, differentiation or maturation of leucocytes or lymphocytes, especially in relation to tissue damage associated with inflammation.
SQ Sequence 193 AA:

Query Match 100.0% Score 33 DB 1 Length 193
Best Local Similarity 100.0% Prod. No. 3.4
Matches 6: Conservative 0: Mismatches 0: Indels 0: Gaps 0
QY 1 FEDMD 6
DB 1111

DB 56 FEDMD 71

RESULT 13
W22044 W22044 standard, peptide, 137 AA.
ID W22044
AC W22044
DE 25-JAN-1998 (first entry)
DE Mouse interferon-gamma inducer protein.
KW Interferon-gamma, IFN-gamma, antiviral, antineoplastic, radiotherapy, immunomodulatory, antitumor agent, chemokine, leukopenia, thrombocytopenia, immunocompetent cells, asthma, hayfever.
KW Chemokine, interleukin, Miller cell.
OS Mus musculus.
PT Key Location/Qualifiers
FT Misc-difference 70
FT /label Met, Thr
FN EF-76778-A1.
PD 09-APR-1997.
PF 26-SEP-1996: JP-269105.
PR 20-SEP-1996: JP-270725.
FR 26-SEP-1996: JP-270725.
FR 29-FEB-1998: JP-067434.
PA (HVA) HAWASHIRAMA SEIBUTSU KAKAYU.
PI Akita K, Fujii M, Kurimoto M, Nakada Y, Tanimoto T.
DR WPI: 97-205381/15.
DR N-PSDB: T60536.
PT Human protein that induces interferon-gamma prodn. in immunocompetent cells - useful for adoptive immunotherapy of tumors and as antimicrobial agent etc.
PS Disclosure, page 22, 25pp, English.
CC The present sequence represents a novel protein from mouse liver cells, which induces interferon-gamma (IFN-gamma) production in immunocompetent cells. This protein enhances cytotoxicity of killer cells and induces their formation. It is used as an antitumor agent for anti-tumor immunotherapy, an antiviral (including anti-AIDS) or antibacterial agent, and in the treatment of allergic or immune system disorders, e.g. asthma, hayfever or rheumatism. When formulated with interleukin-3, it is also used to treat leukopenia and thrombocytopenia associated with radiotherapy or chemotherapy of leukemia and other cancers. When used in anti-tumor immunotherapy, this novel protein significantly improves the therapeutic effect of interferon-gamma. The protein also acts as an adjuvant when administered to the patient (before administration of IFN-2) or by addition to the medium in which cells (intended for return to the patient) are being grown.
SQ Sequence 137 AA:

Query Match 100.0% Score 33 DB 1 Length 157
Best Local Similarity 100.0% Prod. No. 2.7
Matches 6: Conservative 0: Mismatches 0: Indels 0: Gaps 0

QY 1 FEDMD 6
DB 29 FEDMD 34

RESULT 14
W15697 W15697 standard, peptide, 50 AA.
ID W15697
AC W15697
DE 25-JAN-1998 (first entry)
DE N-terminal fragment of interferon gamma inducer protein.
KW Interferon-gamma, IFN-gamma, antiviral, antineoplastic, radiotherapy, immunomodulatory, antitumor agent, chemokine, leukopenia, thrombocytopenia, immunocompetent cells, asthma, hayfever.
KW Chemokine, interleukin, Miller cell.
OS Homo sapiens.
PN EF-76778-A1.
PD 09-APR-1997.
PF 26-SEP-1996: JP-269105.
PR 20-SEP-1996: JP-270725.
FR 26-SEP-1996: JP-270725.

Genome version 4.5
Copyright (c) 1998 - 1999 Compugen Ltd

OM Protein - protein search, using sw model

Run on: June 22, 1999, 10:58:43 : Search time 61.51 Seconds

(without alignments)
3.654 Million cell updates/sec

Title: US-09-030-061-2

Perfect score: 33

Sequence: 1 FECDMD 6

Search: 116788 seqs 37460341 residues

Database:

PIR_581*
1: E111*
2: E112*
3: P111*
4: P114*

Pre: 11.18.19.10.11.12.13.14.15.16.17.18.19.20.21.22.23.24.25.26.27.28.29.30.31.32.33.34.35.36.37.38.39.40.41.42.43.44.45.46.47.48.49.50.51.52.53.54.55.56.57.58.59.60.61.62.63.64.65.66.67.68.69.70.71.72.73.74.75.76.77.78.79.80.81.82.83.84.85.86.87.88.89.90.91.92.93.94.95.96.97.98.99.100.101.102.103.104.105.106.107.108.109.110.111.112.113.114.115.116.117.118.119.120.121.122.123.124.125.126.127.128.129.130.131.132.133.134.135.136.137.138.139.140.141.142.143.144.145.146.147.148.149.150.151.152.153.154.155.156.157.158.159.160.161.162.163.164.165.166.167.168.169.170.171.172.173.174.175.176.177.178.179.180.181.182.183.184.185.186.187.188.189.190.191.192.193.194.195.196.197.198.199.200.201.202.203.204.205.206.207.208.209.210.211.212.213.214.215.216.217.218.219.220.221.222.223.224.225.226.227.228.229.230.231.232.233.234.235.236.237.238.239.240.241.242.243.244.245.246.247.248.249.250.251.252.253.254.255.256.257.258.259.260.261.262.263.264.265.266.267.268.269.270.271.272.273.274.275.276.277.278.279.280.281.282.283.284.285.286.287.288.289.290.291.292.293.294.295.296.297.298.299.300.301.302.303.304.305.306.307.308.309.310.311.312.313.314.315.316.317.318.319.320.321.322.323.324.325.326.327.328.329.330.331.332.333.334.335.336.337.338.339.340.341.342.343.344.345.346.347.348.349.350.351.352.353.354.355.356.357.358.359.360.361.362.363.364.365.366.367.368.369.370.371.372.373.374.375.376.377.378.379.380.381.382.383.384.385.386.387.388.389.390.391.392.393.394.395.396.397.398.399.400.401.402.403.404.405.406.407.408.409.410.411.412.413.414.415.416.417.418.419.420.421.422.423.424.425.426.427.428.429.430.431.432.433.434.435.436.437.438.439.440.441.442.443.444.445.446.447.448.449.450.451.452.453.454.455.456.457.458.459.460.461.462.463.464.465.466.467.468.469.470.471.472.473.474.475.476.477.478.479.480.481.482.483.484.485.486.487.488.489.490.491.492.493.494.495.496.497.498.499.500.501.502.503.504.505.506.507.508.509.510.511.512.513.514.515.516.517.518.519.520.521.522.523.524.525.526.527.528.529.530.531.532.533.534.535.536.537.538.539.540.541.542.543.544.545.546.547.548.549.550.551.552.553.554.555.556.557.558.559.560.561.562.563.564.565.566.567.568.569.570.571.572.573.574.575.576.577.578.579.580.581.582.583.584.585.586.587.588.589.590.591.592.593.594.595.596.597.598.599.600.601.602.603.604.605.606.607.608.609.610.611.612.613.614.615.616.617.618.619.620.621.622.623.624.625.626.627.628.629.630.631.632.633.634.635.636.637.638.639.640.641.642.643.644.645.646.647.648.649.650.651.652.653.654.655.656.657.658.659.660.661.662.663.664.665.666.667.668.669.670.671.672.673.674.675.676.677.678.679.680.681.682.683.684.685.686.687.688.689.690.691.692.693.694.695.696.697.698.699.700.701.702.703.704.705.706.707.708.709.710.711.712.713.714.715.716.717.718.719.720.721.722.723.724.725.726.727.728.729.730.731.732.733.734.735.736.737.738.739.740.741.742.743.744.745.746.747.748.749.750.751.752.753.754.755.756.757.758.759.760.761.762.763.764.765.766.767.768.769.770.771.772.773.774.775.776.777.778.779.780.781.782.783.784.785.786.787.788.789.790.791.792.793.794.795.796.797.798.799.800.801.802.803.804.805.806.807.808.809.810.811.812.813.814.815.816.817.818.819.820.821.822.823.824.825.826.827.828.829.830.831.832.833.834.835.836.837.838.839.840.841.842.843.844.845.846.847.848.849.850.851.852.853.854.855.856.857.858.859.860.861.862.863.864.865.866.867.868.869.870.871.872.873.874.875.876.877.878.879.880.881.882.883.884.885.886.887.888.889.890.891.892.893.894.895.896.897.898.899.900.901.902.903.904.905.906.907.908.909.910.911.912.913.914.915.916.917.918.919.920.921.922.923.924.925.926.927.928.929.930.931.932.933.934.935.936.937.938.939.940.941.942.943.944.945.946.947.948.949.950.951.952.953.954.955.956.957.958.959.960.961.962.963.964.965.966.967.968.969.970.971.972.973.974.975.976.977.978.979.980.981.982.983.984.985.986.987.988.989.990.991.992.993.994.995.996.997.998.999.1000.1001.1002.1003.1004.1005.1006.1007.1008.1009.1010.1011.1012.1013.1014.1015.1016.1017.1018.1019.1020.1021.1022.1023.1024.1025.1026.1027.1028.1029.1030.1031.1032.1033.1034.1035.1036.1037.1038.1039.1040.1041.1042.1043.1044.1045.1046.1047.1048.1049.1050.1051.1052.1053.1054.1055.1056.1057.1058.1059.1060.1061.1062.1063.1064.1065.1066.1067.1068.1069.1070.1071.1072.1073.1074.1075.1076.1077.1078.1079.1080.1081.1082.1083.1084.1085.1086.1087.1088.1089.1090.1091.1092.1093.1094.1095.1096.1097.1098.1099.1100.1101.1102.1103.1104.1105.1106.1107.1108.1109.1110.1111.1112.1113.1114.1115.1116.1117.1118.1119.1120.1121.1122.1123.1124.1125.1126.1127.1128.1129.1130.1131.1132.1133.1134.1135.1136.1137.1138.1139.1140.1141.1142.1143.1144.1145.1146.1147.1148.1149.1150.1151.1152.1153.1154.1155.1156.1157.1158.1159.1160.1161.1162.1163.1164.1165.1166.1167.1168.1169.1170.1171.1172.1173.1174.1175.1176.1177.1178.1179.1180.1181.1182.1183.1184.1185.1186.1187.1188.1189.1190.1191.1192.1193.1194.1195.1196.1197.1198.1199.1200.1201.1202.1203.1204.1205.1206.1207.1208.1209.1210.1211.1212.1213.1214.1215.1216.1217.1218.1219.1220.1221.1222.1223.1224.1225.1226.1227.1228.1229.1230.1231.1232.1233.1234.1235.1236.1237.1238.1239.1240.1241.1242.1243.1244.1245.1246.1247.1248.1249.1250.1251.1252.1253.1254.1255.1256.1257.1258.1259.1260.1261.1262.1263.1264.1265.1266.1267.1268.1269.1270.1271.1272.1273.1274.1275.1276.1277.1278.1279.1280.1281.1282.1283.1284.1285.1286.1287.1288.1289.1290.1291.1292.1293.1294.1295.1296.1297.1298.1299.1300.1301.1302.1303.1304.1305.1306.1307.1308.1309.1310.1311.1312.1313.1314.1315.1316.1317.1318.1319.1320.1321.1322.1323.1324.1325.1326.1327.1328.1329.1330.1331.1332.1333.1334.1335.1336.1337.1338.1339.1340.1341.1342.1343.1344.1345.1346.1347.1348.1349.1350.1351.1352.1353.1354.1355.1356.1357.1358.1359.1360.1361.1362.1363.1364.1365.1366.1367.1368.1369.1370.1371.1372.1373.1374.1375.1376.1377.1378.1379.1380.1381.1382.1383.1384.1385.1386.1387.1388.1389.1390.1391.1392.1393.1394.1395.1396.1397.1398.1399.1400.1401.1402.1403.1404.1405.1406.1407.1408.1409.1410.1411.1412.1413.1414.1415.1416.1417.1418.1419.1420.1421.1422.1423.1424.1425.1426.1427.1428.1429.1430.1431.1432.1433.1434.1435.1436.1437.1438.1439.1440.1441.1442.1443.1444.1445.1446.1447.1448.1449.1450.1451.1452.1453.1454.1455.1456.1457.1458.1459.1460.1461.1462.1463.1464.1465.1466.1467.1468.1469.1470.1471.1472.1473.1474.1475.1476.1477.1478.1479.1480.1481.1482.1483.1484.1485.1486.1487.1488.1489.1490.1491.1492.1493.1494.1495.1496.1497.1498.1499.1500.1501.1502.1503.1504.1505.1506.1507.1508.1509.1510.1511.1512.1513.1514.1515.1516.1517.1518.1519.1520.1521.1522.1523.1524.1525.1526.1527.1528.1529.1530.1531.1532.1533.1534.1535.1536.1537.1538.1539.1540.1541.1542.1543.1544.1545.1546.1547.1548.1549.1550.1551.1552.1553.1554.1555.1556.1557.1558.1559.1560.1561.1562.1563.1564.1565.1566.1567.1568.1569.1570.1571.1572.1573.1574.1575.1576.1577.1578.1579.1580.1581.1582.1583.1584.1585.1586.1587.1588.1589.1590.1591.1592.1593.1594.1595.1596.1597.1598.1599.1600.1601.1602.1603.1604.1605.1606.1607.1608.1609.1610.1611.1612.1613.1614.1615.1616.1617.1618.1619.1620.1621.1622.1623.1624.1625.1626.1627.1628.1629.1630.1631.1632.1633.1634.1635.1636.1637.1638.1639.1640.1641.1642.1643.1644.1645.1646.1647.1648.1649.1650.1651.1652.1653.1654.1655.1656.1657.1658.1659.1660.1661.1662.1663.1664.1665.1666.1667.1668.1669.1670.1671.1672.1673.1674.1675.1676.1677.1678.1679.1680.1681.1682.1683.1684.1685.1686.1687.1688.1689.1690.1691.1692.1693.1694.1695.1696.1697.1698.1699.1700.1701.1702.1703.1704.1705.1706.1707.1708.1709.1710.1711.1712.1713.1714.1715.1716.1717.1718.1719.1720.1721.1722.1723.1724.1725.1726.1727.1728.1729.1730.1731.1732.1733.1734.1735.1736.1737.1738.1739.1740.1741.1742.1743.1744.1745.1746.1747.1748.1749.1750.1751.1752.1753.1754.1755.1756.1757.1758.1759.1760.1761.1762.1763.1764.1765.1766.1767.1768.1769.1770.1771.1772.1773.1774.1775.1776.1777.1778.1779.1780.1781.1782.1783.1784.1785.1786.1787.1788.1789.1790.1791.1792.1793.1794.1795.1796.1797.1798.1799.1800.1801.1802.1803.1804.1805.1806.1807.1808.1809.1810.1811.1812.1813.1814.1815.1816.1817.1818.1819.1820.1821.1822.1823.1824.1825.1826.1827.1828.1829.1830.1831.1832.1833.1834.1835.1836.1837.1838.1839.1840.1841.1842.1843.1844.1845.1846.1847.1848.1849.1850.1851.1852.1853.1854.1855.1856.1857.1858.1859.1860.1861.1862.1863.1864.1865.1866.1867.1868.1869.1870.1871.1872.1873.1874.1875.1876.1877.1878.1879.1880.1881.1882.1883.1884.1885.1886.1887.1888.1889.1890.1891.1892.1893.1894.1895.1896.1897.1898.1899.1900.1901.1902.1903.1904.1905.1906.1907.1908.1909.1910.1911.1912.1913.1914.1915.1916.1917.1918.1919.1920.1921.1922.1923.1924.1925.1926.1927.1928.1929.1930.1931.1932.1933.1934.1935.1936.1937.1938.1939.1940.1941.1942.1943.1944.1945.1946.1947.1948.1949.1950.1951.1952.1953.1954.1955.1956.1957.1958.1959.1960.1961.1962.1963.1964.1965.1966.1967.1968.1969.1970.1971.1972.1973.1974.1975.1976.1977.1978.1979.1980.1981.1982.1983.1984.1985.1986.1987.1988.1989.1990.1991.1992.1993.1994.1995.1996.1997.1998.1999.2000.2001.2002.2003.2004.2005.2006.2007.2008.2009.2010.2011.2012.2013.2014.2015.2016.2017.2018.2019.2020.2021.2022.2023.2024.2025.2026.2027.2028.2029.2030.2031.2032.2033.2034.2035.2036.2037.2038.2039.2040.2041.2042.2043.2044.2045.2046.2047.2048.2049.2050.2051.2052.2053.2054.2055.2056.2057.2058.2059.2060.2061.2062.2063.2064.2065.2066.2067.2068.2069.2070.2071.2072.2073.2074.2075.2076.2077.2078.2079.2080.2081.2082.2083.2084.2085.2086.2087.2088.2089.2090.2091.2092.2093.2094.2095.2096.2097.2098.2099.2100.2101.2102.2103.2104.2105.2106.2107.2108.2109.2110.2111.2112.2113.2114.2115.2116.2117.2118.2119.2120.2121.2122.2123.2124.2125.2126.2127.2128.2129.2130.2131.2132.2133.2134.2135.2136.2137.2138.2139.2140.2141.2142.2143.2144.2145.2146.2147.2148.2149.2150.2151.2152.2153.2154.2155.2156.2157.2158.2159.2160.2161.2162.2163.2164.2165.2166.2167.2168.2169.2170.2171.2172.2173.2174.2175.2176.2177.2178.2179.2180.2181.2182.2183.2184.2185.2186.2187.2188.2189.2190.2191.2192.2193.2194.2195.2196.2197.2198.2199.2200.2201.2202.2203.2204.2205.2206.2207.2208.2209.2210.2211.2212.2213.2214.2215.2216.2217.2218.2219.2220.2221.2222.2223.2224.2225.2226.2227.2228.2229.2230.2231.2232.2233.2234.2235.2236.2237.2238.2239.2240.2241.2242.2243.2244.2245.2246.2247.2248.2249.2250.2251.2252.2253.2254.2255.2256.2257.2258.2259.2260.2261.2262.2263.2264.2265.2266.2267.2268.2269.2270.2271.2272.2273.2274.2275.2276.2277.2278.2279.2280.2281.2282.2283.2284.2285.2286.2287.2288.2289.2290.2291.2292.2293.2294.2295.2296.2297.2298.2299.2300.2301.2302.2303.2304.2305.2306.2307.2308.2309.2310.2311.2312.2313.2314.2315.2316.2317.2318.2319.2320.2321.2322.2323.2324.2325.2326.2327.2328.2329.2330.2331.2332.2333.2334.2335.2336.2337.2338.2339.2340.2341.2342.2343.2344.2345.2346.2347.2348.2349.2350.2351.2352.2353.2354.2355.2356.2357.2358.2359.2360.2361.2362.2363.2364.2365.2366.2367.2368.2369.2370.2371.2372.2373.2374.2375.2376.2377.2378.2379.2380.2381.2382.2383.2384.2385.2386.2387.2388.2389.2390.2391.2392.2393.2394.2395.2396.2397.2398.2399.2400.2401.2402.2403.2404.2405.2406.2407.2408.2409.2410.2411.2412.2413.2414.2415.2416.2417.2418.2419.2420.2421.2422.2423.2424.2425.2426.2427.2428.2429.2430.2431.2432.2433.2434.2435.2436.2437.2438.2439.2440.2441.2442.2443.2444.2445.2446.2447.2448.2449.2450.2451.2452.2453.2454.2455.2456.2457.2458.2459.2460.2461.2462.2463.2464.2465.2466.2467.2468.2469.2470.2471.2472.2473.2474.2475.2476.2477.2478.2479.2480.2481.2482.2483.2484.2485.2486.2487.2488.2489.2490.2491.2492.2493.2494.2495.2496.2497.2498.2499.2500.2501.2502.2503.2504.2505.2506.2507.2508.2509.2510.2511.2512.2513.2514.2515.2516.2517.2518.2519.2520.2521.2522.2523.2524.2525.2526.2527.2528.2529.2530.2531.2532.2533.2534.2535.2536.2537.2538.2539.2540.2541.2542.2543.2544.2545.2546.2547.2548.2549.2550.2551.2552.2553.2554.2555.2556.2557.2558.255

[illegible][illegible][illegible]

```

Query Match# 87,981  Score 29  E-Value 372,
Pair Local Similarity 92.39%  Prod No 261
Matches 51  Conservative 11  Mismatches 0  Gaps 0

Q# 1  SEQID 6
      111
      111
DB 26  SEQID 31

RESULT 8
S19702
Fibronectin-Binding Protein B, Staphylococcus aureus
C-Species: Staphylococcus aureus
C-ID:PA13-140166  Sequence_Revision 13-Jan-1995  #ext_change 06-Sep-1997
C-Accession: S19702
Reference: K. Nakano, C. Mueller, H. P. Lindberg, M.
Ehrig, J. Bickham, and J. G. Boring, 1991
A title for this record should fibronectin binding proteins in Staphylococcus aureus
A preferred name for this record: M19702.M19702
Accession: S19702
A status: preliminary
A molecule type: DNA
A residues: 1940  CORD
A cross references: PDB: Y6999, NID: J03140, EMB: J521502
C keywords: fibronectin binding

```

Only Month	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400
Only Month	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76																																																																																																																																																																																																																																																																																																																															

RESULT 9

[illegible]

R Murakami, Y Nakatsu, M Hattawa, E Shibata, T Ozawa, M Sasahara & S Sakai
Submitted to the EMBL Data Library May 1995
A.TS-0176-A-1898-1
A.Facility number: S56185
Accession: 556185

A: Molecule type: DNA
A: Residues: 1,131 <MB>
A: Cross-references: EMBL: E55017; NBR: 85866; EMBL: 000044; EMBL: 000077; EMBL: 00356; EMBL: 00357
R: Masters: B.S. Stohl, L.L. Clayton, D.A. Cell 51, 89-99, 1987
A: Title: Yeast mitochondrial DNA: organization, inheritance and function
A: Reference: Number: A7335; Title: 8000333

[illegible]

A:Stratig: nucleic acid sequence not shown; translation not shown
 A:Molecular type: DNA
 A:Accession: U03575.1
 A:Cross-references: EMBL D44538; NID 877193; EDB000610; PIR027193
 A:Note: The nucleic acid sequence was submitted to the EMBL Data Library, December 1994
 C:Genetics:
 A:Gene: SGP;RPO41
 A:Cross-references: SGD:S0001858; MIPS:YDL036w

Query Match	Score	DP	Posit	Score	
Best Local Similarity	87.8	23	2	10.5	
Matches	5	Conservative	1	Mismatches	0
				Gaps	0

QY	1	FEDMTD	6
		11:11	
DB	1300	FEDMTD	1305
RESULT 10			
S37845			
NATURALGAS			

Species: *Saccharomyces cerevisiae*
 A.Variety: strain 2182
 C.Date: 23-Feb-1995 RefSeq accession: S7845 change 06-Feb-1998
 C.Accession: S7845; A55465; C5465
 R.Rieger, M.
 Submitted to the Protein Sequence Database, March 1994
 A.Reference number: S7845
 A.Accession: S7845
 A.Molecule type: DNA

[illegible]

A:Rimst, S., Nagasawa, N., Meserli, J., Albertini, A.M., Arcene, G., Arcene, J.B.,
 A:Kron, S., Boullier, L., S., Brusch, C.V., Caldwell, R., Caputo, V., Gabor, N.M.,
 A: Ehlich, S.D., Emerson, P.J., Entian, K.D., Ettimann, J., Fabbro, D., Fournier,
 Nature 360, 449-450, 1997
 A:Authors: Filiz, C., Fujita, M., Fujita, Y., Fuma, S., Galiizi, A., Galov, N.,
 Wood, C.R., Henalt, C., Hilbert, H., Holasap, S., Hosono, S., Hilo, M., Hiron,
 Koningsstein, G., Krogh, S., Kuroki, M., Kurla, K., Lapins, A., Lario, S., Lario,
 A:Authors: Lazarevic, V., Lee, S.M., Levine, A., Liu, H., Masuda, S., Mave, S.,
 K., Ohtsuka, A., Oudga, B., Park, S.H., Parro, A., Pohl, T.M., Potteville, P.,
 Rivola, C., Roeha, P., Roeha, P., Rosso, M., Sable, Y., Sato, T., Scharf, E.,
 A:Authors: Schreier, R., Scifone, R., Sakai, J., Sakai, A., Sakai, A., Sakai,
 amasoshi, A., Tanaka, T., Tetsura, P., Tognoni, A., Tosto, V., Uchiyama, S.,
 A:Authors: Yamada, H., Yamada, K., Yamada, Y., Yoda, S., Yoshida, K.,
 A:Authors: Zamsler, E., Yoshikawa, H., Zanchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus*
 A:Reference number: A694600.m01136044033
 A:Accession: F59878
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1363 (KUN)
 A:Cross-references: GR 29919, GE A099216, NID 3253102, EEA 0000016, EEA 0000017
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: ylon
 A:Superfamily: conserved hypothetical protein H10345

Query Match: 84.8% Score 28, EB 2, Length 363,
Best Local Similarity: 84.8% Pred. No. 59;
Matches: 51 Conservative: 17 Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 FEDMTD 4
11111
Db 57 FEDMTD 42

RESULT 15

S64082

Probably membrane protein (G31375) Yeast (Saccharomyces cerevisiae)

Na: Alternate names: hypothetical protein G3139

C: Species: Saccharomyces cerevisiae

C: Date: 17 May 1996 #sequence_revision 17 May 1996 #text_change 14-Nov-1997

C: Accession: S64082

R: Rieger, M.; Mueller-Auer, S.; Bruckner, M.; Schaefer, M.

submitted to the Protein Sequence Database, May 1996

A: Reference number: S64071

A: Accession: S64082

A: Molecule type: DNA

A: Residues: 1387 R: EDS

A: 1158-1387: DMBL27597, NID_132289, EIL_243961, EID_432289, MFS_N10710

A: Experimental source: strain S286C

C: Genes:

A: Map position: 7L

C: Keywords: transmembrane protein

E311-277: G-protein, 1158-1387: #62716 predicted TMN

Query Match: 84.8% Score 28, DB 2, Length 387;
Best Local Similarity: 83.3% Pred. No. 63;

Matches: 51 Conservative: 0; Mismatches: 1; Indels: 0; Gaps: 0;

QY 1 FEDMTD 4
11111

Db 361 FEDMTD 366

Search completed: June 22, 1999, 10:58:45
Job time: 14 sec



GenCorp visting 4 5
Copyright (c) 1993 - 1998 CompuGen Ltd.

OM protein protein search, using sw model

Run on: Tue 22, 1999, 10:59:41 : Search time 45.16 seconds

(without alignments)
3.566 Million cell updates/sec

Title: US-09-030-061-2

Perfect score: 32

Sequence: 1 FEDMD 6

Scoring table: 21500002

Search: 74013 seqs, 26840235 residues

Database: SwissProt_36.*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	193	1 IL18_HUMAN	Q14116 homo sapien
2	33	100.0	192	1 IL18_MOUSE	P03840 mus musculu
3	30	90.9	862	1 YMR4_GAEEL	P32742 saccharobact
4	29	87.9	1071	1 PPI6_YEAST	P15698 saccharomyce
5	28	87.9	754	1 RAD4_YEAST	P14796 saccharomyce
6	28	87.9	1351	1 FROM_YEAST	P34433 saccharomyce
7	28	87.9	482	1 TEA_YEAST	P26160 saccharomyce
8	28	87.9	1450	1 LEM1_EUPHR	U06183 euphates cr
9	28	87.9	445	1 PICH_CHILI	U08252 chloebium
10	28	87.9	387	1 YOH1_YEAST	P33159 saccharomyce
11	28	87.9	323	1 YOH1_BACCU	Q04017 bacillus su
12	28	87.9	323	1 YOH1_YEAST	P30077 saccharomyce
13	27	81.8	451	1 GRI1_YEAST	P39958 saccharomyce
14	27	81.8	451	1 HDAL_GAEEL	Q17695 caenorhabdi
15	27	81.8	160	1 IL18_PIG	Q19073 sus scrofa
16	27	81.8	194	1 IL18_PAT	P07636 felis domest
17	27	81.8	194	1 IL18_HUMAN	P33708 homo sapien
18	27	81.8	194	1 NCL_MOUSE	P38129 drosophila
19	27	81.8	365	1 RRM9_YEAST	P33437 saccharomyce
20	27	81.8	130	1 UD3_HSV1	P10217 herpes simp
21	27	81.8	1559	1 VIL3_ONCV	Q92093 oncorhynch
22	27	81.8	356	1 VHR_HSV60	Q01346 herpes simp
23	27	81.8	1166	1 XMR_XIPPA	P33388 xiphophorus
24	27	81.8	143	1 YAM_RHISN	P33360 thizobium s
25	27	81.8	531	1 YOCG_PACSO	P45942 bacillus su
26	27	81.8	115	1 YXEA_BACSU	P54940 bacillus su
27	27	81.8	222	1 AWYR_SEGGE	P20271 seggiu cere
28	26	78.8	856	1 CLPB_HELPY	P11404 heliocoacte
29	26	78.8	856	1 CNRA_BOVIN	P11411 bos taurus
30	26	78.8	856	1 CNRA_HUMAN	P11412 canis fami
31	26	78.8	856	1 CNRA_HUMAN	P11413 canis fami
32	26	78.8	856	1 CNRA_HUMAN	P11414 canis fami
33	26	78.8	856	1 CNRA_HUMAN	P11415 canis fami
34	26	78.8	856	1 CNRA_HUMAN	P11416 canis fami
35	26	78.8	856	1 CNRA_HUMAN	P11417 canis fami
36	26	78.8	856	1 CNRA_HUMAN	P11418 canis fami
37	26	78.8	856	1 CNRA_HUMAN	P11419 canis fami
38	26	78.8	856	1 CNRA_HUMAN	P11420 canis fami
39	26	78.8	856	1 CNRA_HUMAN	P11421 canis fami
40	26	78.8	856	1 CNRA_HUMAN	P11422 canis fami
41	26	78.8	856	1 CNRA_HUMAN	P11423 canis fami
42	26	78.8	856	1 CNRA_HUMAN	P11424 canis fami
43	26	78.8	856	1 CNRA_HUMAN	P11425 canis fami
44	26	78.8	856	1 CNRA_HUMAN	P11426 canis fami
45	26	78.8	856	1 CNRA_HUMAN	P11427 canis fami

ALIGNMENTS

44	26	78.8	1276	1 MDRL_CRIGR	P21448 cricetus
45	26	78.8	1276	1 MDRL_MOUSE	P21447 mus musculu

RESULT 1	IL18_HUMAN	STANDARD	PRT	193 AA.
AC	Q14116:			
DT	15-JUL-1998 (REL. 36, CREATED)			
DI	15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)			
DE	15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)			
DE	INTERFERON-18 PRECURSOR (IL-18) (INTERFERON-GAMMA INDUCING FACTOR)			
TE	(HUMAN-GAMMA-INDUCING FACTOR), (INTERFERON-1 GAMMA) (IL-1 GAMMA).			
GN	IL18 OR IL1F.			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA			
OC	EUTHERIA; PRIMATES.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=LIVER;			
PX	MEDLINE: 95247646.			
PA	USHIO S., NAMBA M., OKURA T., HATTORI K., NIKADA Y., AKITA K.,			
PA	TANABE F., KONISHI K., MICHAEL M., FUJII M., TORIIDE K., TANIKAWA T.,			
PA	FUKUDA S., IKEDA M., OKAMURA H., KUBIMOTO M.,			
RL	J. IMMUNOL. 156:4274-4279(1996).			
RN	[2]			
RP	SEQUENCE OF 2193 FROM N.A.			
RC	TISSUE=PERIPHERAL BLOOD;			
PA	CONTI R., KIM S.J., LINI C., CHUN H.S., JOH T.H.,			
PA	SUMITZER JEPF-1997, 75 PMOL-GENE/ANALYSIS DATA BANKS			
CC	- FUNCTION: ARGUMENTS: NATURAL KILLER CELL ACTIVITY IN SPLEN CELLS			
CC	AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HIFER TYPE 1			
CC	CELLS.			
TE	EMBL: D49450, G1405419; 1			
DR	EMBL: U04344, G1899242; 1			
DR	KIM: 6809923; 1			
KW	CYTOKINE.			
ET	PROPER			
FI	CHAIN			
SV	SEQUENCE 193 AA; 22426 MW; 7855271 GC(23)			

Query Match	Score 33; DB 1; Length 193;
Best Local Similarity	100.0%;
Best Local Similarity	100.0%;
Matches	6; Conservative 0; Mismatched 0; Indels 0; Gaps 0;

QY	1 FEDMD 6
DB	66 FEDMD 71

RESULT 2	IL18_MOUSE	STANDARD	FEF	192 AA.
AC	P70380:			
DT	15-JUL-1998 (REL. 36, CREATED)			
DI	15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)			
DE	15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)			
DE	INTERFERON-18 PRECURSOR (IL-18) (INTERFERON-GAMMA INDUCING FACTOR)			
TE	(HUMAN-GAMMA-INDUCING FACTOR), (INTERFERON-1 GAMMA) (IL-1 GAMMA).			
GN	IL18 OR IL1F.			
OS	MUS MUSCULUS (MOUSE).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA			
OC	EUTHERIA; RODENTIA.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=LIVER;			
PX	MEDLINE: 9601009.			
PA	OKAMURA H., KONISHI K., MICHAEL M., FUJII M., TORIIDE K., TANIKAWA T.,			
PA	FUKUDA S., IKEDA M., OKAMURA H., KUBIMOTO M.,			
PA	J. IMMUNOL. 156:4274-4279(1996).			

RC SIRAIN=168;
RA FOULGER D., ERRINGTON J.

11 19... PER... (LAST SEQUENCE UPDATED)
 12 19... PER... (LAST SEQUENCE UPDATED)
 13 19... PER... (LAST SEQUENCE UPDATED)
 14 19... PER... (LAST SEQUENCE UPDATED)

15 19... PER... (LAST SEQUENCE UPDATED)

16 19... PER... (LAST SEQUENCE UPDATED)

17 19... PER... (LAST SEQUENCE UPDATED)

18 19... PER... (LAST SEQUENCE UPDATED)

19 19... PER... (LAST SEQUENCE UPDATED)

20 19... PER... (LAST SEQUENCE UPDATED)

21 19... PER... (LAST SEQUENCE UPDATED)

22 19... PER... (LAST SEQUENCE UPDATED)

23 19... PER... (LAST SEQUENCE UPDATED)

24 19... PER... (LAST SEQUENCE UPDATED)

25 19... PER... (LAST SEQUENCE UPDATED)

26 19... PER... (LAST SEQUENCE UPDATED)

27 19... PER... (LAST SEQUENCE UPDATED)

28 19... PER... (LAST SEQUENCE UPDATED)

29 19... PER... (LAST SEQUENCE UPDATED)

30 19... PER... (LAST SEQUENCE UPDATED)

31 19... PER... (LAST SEQUENCE UPDATED)

32 19... PER... (LAST SEQUENCE UPDATED)

33 19... PER... (LAST SEQUENCE UPDATED)

34 19... PER... (LAST SEQUENCE UPDATED)

35 19... PER... (LAST SEQUENCE UPDATED)

36 19... PER... (LAST SEQUENCE UPDATED)

37 19... PER... (LAST SEQUENCE UPDATED)

38 19... PER... (LAST SEQUENCE UPDATED)

39 19... PER... (LAST SEQUENCE UPDATED)

40 19... PER... (LAST SEQUENCE UPDATED)

41 19... PER... (LAST SEQUENCE UPDATED)

42 19... PER... (LAST SEQUENCE UPDATED)

43 19... PER... (LAST SEQUENCE UPDATED)

44 19... PER... (LAST SEQUENCE UPDATED)

45 19... PER... (LAST SEQUENCE UPDATED)

46 19... PER... (LAST SEQUENCE UPDATED)

47 19... PER... (LAST SEQUENCE UPDATED)

48 19... PER... (LAST SEQUENCE UPDATED)

49 19... PER... (LAST SEQUENCE UPDATED)

50 19... PER... (LAST SEQUENCE UPDATED)

51 19... PER... (LAST SEQUENCE UPDATED)

52 19... PER... (LAST SEQUENCE UPDATED)

53 19... PER... (LAST SEQUENCE UPDATED)

54 19... PER... (LAST SEQUENCE UPDATED)

55 19... PER... (LAST SEQUENCE UPDATED)

56 19... PER... (LAST SEQUENCE UPDATED)

57 19... PER... (LAST SEQUENCE UPDATED)

58 19... PER... (LAST SEQUENCE UPDATED)

59 19... PER... (LAST SEQUENCE UPDATED)

60 19... PER... (LAST SEQUENCE UPDATED)

Search completed: June 22, 1999, 10:59:42
 Job time: 58 sec

GenCorp version 4.5
Copyright (c) 1993 - 1998 CompuGen Ltd.

CM protein protein search, using sw model

Run on: June 22, 1999, 10:59:42 : Search time 45.16 seconds

(without alignments)
4.160 Million cell updates/sec

File: US-09-030-061-3

Perfect score: 33

Sequence: 1 FRILINK 7

Search: 11979 vops 2949000 residues

Database: SwissProt_36

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	193	1 IL18_HUMAN	Q14116 homo sapien
2	32	100.0	192	1 IL18_MOUSE	P31918 mus muscula
3	32	97.0	215	1 CYA1_POTAN	Q01513 pedoscopa d
4	32	97.0	215	1 CYA1_POTAN	Q01513 pedoscopa d
5	32	97.0	215	1 CYA1_POTAN	Q01513 pedoscopa d
6	32	97.0	215	1 CYA1_POTAN	Q01513 pedoscopa d
7	32	97.0	215	1 CYA1_POTAN	Q01513 pedoscopa d
8	32	97.0	215	1 CYA1_POTAN	Q01513 pedoscopa d
9	32	97.0	215	1 CYA1_POTAN	Q01513 pedoscopa d
10	32	97.0	215	1 CYA1_POTAN	Q01513 pedoscopa d
11	32	97.0	215	1 CYA1_POTAN	Q01513 pedoscopa d
12	32	97.0	215	1 CYA1_POTAN	Q01513 pedoscopa d
13	32	97.0	215	1 CYA1_POTAN	Q01513 pedoscopa d
14	32	97.0	215	1 CYA1_POTAN	Q01513 pedoscopa d
15	32	97.0	215	1 CYA1_POTAN	Q01513 pedoscopa d
16	32	97.0	215	1 CYA1_POTAN	Q01513 pedoscopa d
17	32	97.0	215	1 CYA1_POTAN	Q01513 pedoscopa d
18	32	97.0	215	1 CYA1_POTAN	Q01513 pedoscopa d
19	32	97.0	215	1 CYA1_POTAN	Q01513 pedoscopa d
20	32	97.0	215	1 CYA1_POTAN	Q01513 pedoscopa d
21	32	97.0	215	1 CYA1_POTAN	Q01513 pedoscopa d
22	32	97.0	215	1 CYA1_POTAN	Q01513 pedoscopa d
23	32	97.0	215	1 CYA1_POTAN	Q01513 pedoscopa d
24	32	97.0	215	1 CYA1_POTAN	Q01513 pedoscopa d
25	32	97.0	215	1 CYA1_POTAN	Q01513 pedoscopa d
26	32	97.0	215	1 CYA1_POTAN	Q01513 pedoscopa d
27	32	97.0	215	1 CYA1_POTAN	Q01513 pedoscopa d
28	32	97.0	215	1 CYA1_POTAN	Q01513 pedoscopa d
29	32	97.0	215	1 CYA1_POTAN	Q01513 pedoscopa d
30	32	97.0	215	1 CYA1_POTAN	Q01513 pedoscopa d
31	32	97.0	215	1 CYA1_POTAN	Q01513 pedoscopa d
32	32	97.0	215	1 CYA1_POTAN	Q01513 pedoscopa d
33	32	97.0	215	1 CYA1_POTAN	Q01513 pedoscopa d
34	32	97.0	215	1 CYA1_POTAN	Q01513 pedoscopa d
35	32	97.0	215	1 CYA1_POTAN	Q01513 pedoscopa d
36	32	97.0	215	1 CYA1_POTAN	Q01513 pedoscopa d
37	32	97.0	215	1 CYA1_POTAN	Q01513 pedoscopa d
38	32	97.0	215	1 CYA1_POTAN	Q01513 pedoscopa d
39	32	97.0	215	1 CYA1_POTAN	Q01513 pedoscopa d
40	32	97.0	215	1 CYA1_POTAN	Q01513 pedoscopa d
41	32	97.0	215	1 CYA1_POTAN	Q01513 pedoscopa d
42	32	97.0	215	1 CYA1_POTAN	Q01513 pedoscopa d
43	32	97.0	215	1 CYA1_POTAN	Q01513 pedoscopa d

44 26 78.8 154 1 YVAN_BACUS
45 25 77.8 153 1 YVAN_BACUS

ALIGNMENTS

RESULT 1
IL18_HUMAN STANDARD: PRT: 193 AA.
AC Q14116:
DI 15-JUL-1998 (REL. 35) (CREATED)
DI 15-JUL-1998 (REL. 35) (LAST SEQUENCE UPDATE)
DI 15-JUL-1998 (REL. 35) (LAST ANNOTATION UPDATE)
DI INTERFERON-16 PREPROPEPTIDE (17-16) (INTERFERON-GAMMA INDUCING FACTOR)
DI (HFN-GAMMA-INDUCING FACTOR) (INTERFERON-1 GAMMA) (G171 GAMMA).
GN IL18 OR IGIF.
OS HOMO SAPIENS (HUMAN).
OC ERYTHROCYTES, METASTAS, CHELATA, VERTEBRATA, TETRAPODA, MAMMALIA.
OC ERYTHROCYTES, PRIMATES.
RN (1)
RP SOURCE FROM N.A.
RC TISSUE=LIVER;
FX MELLINE; 25443946.
FX USHTO S. NAKABA M. OKURA T. HATTORI K. NIKAWA Y. AKITA K.
PA TANABE Y. KONISHI K. MIZUTANI M. FUJII M. TOSHIKAZU K. TANIMOTO T.
PA FUKUDA S. IKEDA M. OKAMURA H. KURIMOTO M.
RL J. IMMUNOL. 156:4274-4279(1996).
RN (2)
RP SOURCE OF 2-193 FROM N.A.
RC TISSUE=PERIPHERAL BLOOD;
FX GENTIL H. KIM S.J. JINJI G. CHUN H.S. JOH T.H.
RL STRATFIELD (FEB-1997) IN EMBL/GENBANK/DBJ DATA BANKS.
CC FUNCTION: AGENTS: NATURAL KILLER CELL ACTIVITY IN SPLEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE 1
CC CELLS.
EX EMBL: 149350, Q1405319;
EX EMBL: 090131, Q1992912;
EX MIM: 600453;
KM CYTOKINE.
FT PROPEP
FT CHAIN 27 192 BY SIMILARITY.
SC SEQUENCE 193 AA. 2500 MW. 788117 CYS002

Query Match: 100.0% Score 33, DB 1, Length 193
Post Local Similarity 100.0%, Pred. No. 0.8
Matches: 0, Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 1 FRILINK 7
DB 170 FRILINK 176

RESULT 2
IL18_MOUSE
AC P31918:
DI 15-JUL-1998 (REL. 35) (CREATED)
DI 15-JUL-1998 (REL. 35) (LAST SEQUENCE UPDATE)
DI 15-JUL-1998 (REL. 35) (LAST ANNOTATION UPDATE)
DI INTERFERON-16 PREPROPEPTIDE (17-16) (INTERFERON-GAMMA INDUCING FACTOR)
DI (HFN-GAMMA-INDUCING FACTOR) (INTERFERON-1 GAMMA) (G171 GAMMA).
GN IL18 OR IGIF.
OS MUS MUSCULUS (MURINE).
OC ERYTHROCYTES, METASTAS, CHELATA, VERTEBRATA, TETRAPODA, MAMMALIA.
OC ERYTHROCYTES, PRIMATES.
RN (1)
RP SOURCE FROM N.A. AND PARTIAL SEQUENCE.
RC TISSUE=LIVER;
FX MEDLINE: 96061809.
FX OKAMURA H. TANABE Y. KONISHI K. MIZUTANI M. FUJII M. TOSHIKAZU K. TANIMOTO T.
PA FUKUDA S. IKEDA M. OKAMURA H. KURIMOTO M.


```
CC      -1- CATALYTIC ACTIVITY: Nucleoside triphosphatase, N triphosphatase (NANP).
CC      -1- THIS RNA POLYMERASE IS ENCODED ON A CHROMOSOME.
CC      -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
DR      EMBL: X78541; G587604; .
DR      EMBL: X52177; G98801; .
DR      EMBL: X95275; E220241; .
DR      PIR: S10438; RNZORF.
DR      PROSITE: PS01166; RNA_POL_BETA_1.
KM      TRANSCRIPTION: DNA-DIRECTED RNA POLYMERASE.
SC      SEQUENCE: 1198 AA; 12195 MW; 59EAFPEI CDD12;

Query Match:          87.9% Score 23; ID 1; Length 1024;
Host Local Similarity: 85.7%; Prot No 27;
Matches:    60 Correspondence: 1; Mismatches: 0; Indels: 0; Gaps: 0

QY      1 FRILIER 7
        |||||:
DB      988 FRILIER 994

RESULT 8
SYDC_CAEEL STANDARD: PRI: 1198 AA.
AC      VU9390;
DT      01-OCT-1996 (REL. 34) (CREATED)
DI      01-OCT-1996 (REL. 34) (LAST SEQUENCE UPDATE)
DT      15-JUN-1998 (REL. 35) (LAST ANNOTATION UPDATE)
FE      PRERNALE LEUCOTRINA SYNTHETASE (EC 6.1.1.14) (LEUCINE TRANA LIGASE)
DE      (LEURS) :
CS      R74.1.
OS      CAENOBACTHIDIS ELEGANS.
CC      EVANGELICA, METABOLA, ACILLIMOLAS, NEVATICA, DEFERENTIA, EMULITICA.
RN      [1]
RC      SEQUENCE OF 1,179 FROM N.A.
RA      STRAIN=BRISTOL N2;
GC      GARDINER A.;
CS      FORM:1111; (FORM:1111) 1. EMBL: X95275; G577554; .
RN      [2]
RC      SEQUENCE OF 641,1109 FROM N.A.
RA      STRAIN=BRISTOL N2;
BA      LLOYD C.;
PR      SUBMITTED (NOV-1994) TO EMBL/GENBANK/EBI DATA BANKS.
CC      -1- CATALYTIC ACTIVITY: ATP + L-LEUCINE + IRNA(LEO) = AMP + PYROPHOSPHATE + L-LEUCYL-IRNA(LEO) .
CC      -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
DR      EMBL: Z39238; GI687049; .
DR      EMBL: Z46787; G577554; .
LR      WORMHEIM; R74.1.1.C216317.
DR      PROSITE: PS00186; AA_IHNA_LIGASE_1.
VM      AMINOACYL-TRNA SYNTHETASE; PROTEIN BIOSYNTHESIS; LIGASE; ATP BINDING.
FT      SIMILAR 50 60 "HIGH" REGION.
LM      SIMILAR 73 84 *WVSST* PEPTON.
LT      BINDING 733 733 ATP (BY SIMILARITY) .
SC      SEQUENCE 1198 AA; 126190 MW; 74166501 CDD12;
```


Accession	Gene	Accession	Gene
42	Mouse interferon-	42	Mouse interferon-
43	Mouse interferon-	43	Mouse interferon-
518	Mouse interferon-	518	Mouse interferon-
63.5	Mouse interferon-	63.5	Mouse interferon-
157	Mouse interferon-	157	Mouse interferon-
1	Mouse interferon-	1	Mouse interferon-
W15704	Mouse interferon-	W15704	Mouse interferon-

10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	-----

FT	Region	41.	.47

FT	Region	41.	.47

25-FEB-1997; JP-055468.
 PA (HAYB) HAYASHIBARA SEIMITSU KAGAKU
 PI Gillespie M, Herndon NJ, Kunitama M, Udagawa N
 DP WPI: 98-44864/39.
 DR N-PSDB: V19226.
 QY Use of interleukin-18 to inhibit osteoclast formation - in treatment
 PI of e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome.
 PT osteoclastoma, chronic rheumatoid arthritis, deformity osteitis,
 PI primary hyperthyroidism and osteoporosis
 PS Claim 4: Page 18; 56pp; English.
 CC Interleukin-18 (IL-18) or a functional equivalent can be used for
 CC inhibition of osteoclast formation. IL-18 is used for treating or
 CC preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma
 CC Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid
 CC arthritis, deformity osteitis, primary hyperthyroidism, osteopenia and
 CC osteoporosis.
 SO Sequence 157 AA:

Query Match 100.0% Score 816; DB 1; Length 157.
 Best Local Similarity 100.0%; Pred. No. 4.7e-83;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFVKLSKSVNINNVVLTGNNPPEFMDSCDNPATFIFISWYISQPHKM 60
 DB 1 YFVKLSKSVNINNVVLTGNNPPEFMDSCDNPATFIFISWYISQPHKM 60
 QY 51 AVIISVTVKIVNLSNPNKISKKNNPNPVTKSTIFFGVSVPDQNMKPFESSY 120
 DB 61 AVIISVTVKIVNLSNPNKISKKNNPNPVTKSTIFFGVSVPDQNMKPFESSY 120
 QY 121 EGYFLAGEKPEFLFKILKKEDEGDSIMFTVONED 157
 DB 121 EGYFLAGEKPEFLFKILKKEDEGDSIMFTVONED 157

RESULT 5
 W77082
 ID W77082 standard protein 193 AA.
 AC W77082:
 DT 16-NOV-1998 (first entry)
 DE Interleukin 18 active protein and precursor
 KW Human; interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;
 KW osteoclastoma; Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;
 KW chronic rheumatoid arthritis; deformity osteitis; primary hyperthyroidism;
 OS Homo sapiens.
 FH Key: Location/Qualifiers
 FT Peptide 1..36
 FT /note="Signal peptide"
 FT Peptide 37..193
 FT /note="Full length protein"
 PN EP-91662-AA.
 PD 22-SEP-1998.
 PE 22-SEP-1998; 561955.
 PI 25-FEB-1997; JP-055468.
 PA (HAYB) HAYASHIBARA SEIMITSU KAGAKU
 PI Gillespie M, Herndon NJ, Kunitama M, Udagawa N
 DP WPI: 98-44864/39.
 DR N-PSDB: V4828.
 PT Use of interleukin-18 to inhibit osteoclast formation - in treatment
 PI of e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome,
 PI osteosarcoma, chronic rheumatoid arthritis, deformity osteitis,
 PI primary hyperthyroidism and osteoporosis
 PS Disclosure: Page 24-28; 66pp; English.
 CC Interleukin 18 (IL-18) or a functional equivalent can be used for
 CC inhibition of osteoclast formation. IL-18 is used for treating or
 CC preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma
 CC Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid
 CC arthritis, deformity osteitis, primary hyperthyroidism, osteopenia and
 CC osteoporosis.
 SO Sequence 193 AA:

Query Match 99.4% Score 813; DB 1; Length 193.
 Best Local Similarity 99.4%; Pred. No. 1.3e-83;
 Matches 193; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFVKLSKSVNINNVVLTGNNPPEFMDSCDNPATFIFISWYISQPHKM 60
 DB 37 YFVKLSKSVNINNVVLTGNNPPEFMDSCDNPATFIFISWYISQPHKM 56
 QY 61 AVIISVTVKIVNLSNPNKISKKNNPNPVTKSTIFFGVSVPDQNMKPFESSY 120
 DB 57 AVIISVTVKIVNLSNPNKISKKNNPNPVTKSTIFFGVSVPDQNMKPFESSY 126
 QY 121 EGYFLAGEKPEFLFKILKKEDEGDSIMFTVONED 157
 DB 157 EGYFLAGEKPEFLFKILKKEDEGDSIMFTVONED 193

RESULT 6
 ID R99564 standard protein 157 AA.
 AC R99564:
 DT 29-SEP-1996 (first entry)
 DE Human interferon-gamma inducer protein.
 KW Interferon gamma inducer protein; IFN-gamma; antiviral; virucide;
 KW antitumour; antibacterial; immunoregulator; adoptive immunotherapy;
 KW therapy; cancer.
 OS Homo sapiens.
 FH Key: Location/Qualifiers
 FT misc-difference 73
 FT /label= Ile, Thr
 PN EP-712931-A2.
 PD 22-MAY-1996.
 PE 10-NOV-1995; 408055.
 PI 15-NOV-1994; JP-0582403.
 PR 23-FEB-1995; JP-058240.
 PR 10-MAR-1995; JP-078357.
 PR 18-SEP-1995; JP-262062.
 PR 29-SEP-1995; JP-274988.
 PA (HAYB) HAYASHIBARA SEIMITSU KAGAKU
 PI Fukuda S, Kohno K, Kunitama T, Kunitama M, Okamura H;
 PI Taniguchi M, Yamamoto T, Torioka K, Ushio S;
 PE WPI: 96-25837/26.
 DR N-PSDB: T32411.
 FT CNA encoding interferon-gamma protein, inducing polypeptide - useful
 FT to treat and prevent, e.g. viral disease, malignancies and immune
 PT disorders
 PS Example P-1-1: Page 28; 48pp; English.
 CC A novel human protein (R99564) that induces interferon-gamma
 CC (IFN-gamma) production by immunocompetent cells is the product of a
 CC phage cDNA clone (T32411) derived from a human liver library.
 CC PCR amplification of the cDNA (see also T32409-10) and expression
 CC in Escherichia coli XL1 Blue MRF'kan allowed production of recombinant
 CC inducer protein. This was used to construct hybridoma H 1, which
 CC produced anti-IFN-gamma inducer protein monoclonal antibody H-1mAb,
 CC useful in the detection and purification of the inducer protein
 CC (see also R99558).
 SO Sequence 157 AA:

Query Match 99.4% Score 811; DB 1; Length 157.
 Best Local Similarity 99.4%; Pred. No. 1.7e-82;
 Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFVKLSKSVNINNVVLTGNNPPEFMDSCDNPATFIFISWYISQPHKM 60
 DB 1 YFVKLSKSVNINNVVLTGNNPPEFMDSCDNPATFIFISWYISQPHKM 50
 QY 61 AVIISVTVKIVNLSNPNKISKKNNPNPVTKSTIFFGVSVPDQNMKPFESSY 120
 DB 61 AVIISVTVKIVNLSNPNKISKKNNPNPVTKSTIFFGVSVPDQNMKPFESSY 120
 QY 121 EGYFLAGEKPEFLFKILKKEDEGDSIMFTVONED 157
 DB 121 EGYFLAGEKPEFLFKILKKEDEGDSIMFTVONED 157

PA (HAY) HAYASHIBARA SEIBUTSU KAGAKU.
 DR WPI: 97-369341/34.
 DR N-PSDB: 180205.
 PT A drug containing a polypeptide which induces interferon-gamma -
 PT useful for treating e.g. malignant tumours, viral, bacterial or
 PT immune diseases.
 PS Claim 1: Page 9: 12pp; Japanese.
 CC This sequence represents a protein which induces interferon-gamma
 CC production in immunocompetent cells. This protein may be used as
 CC the major component in a drug for the prevention and treatment of
 CC e.g. malignant tumours, viral diseases, bacterial infections and
 CC immune diseases.
 SO Sequence 157 AA:

Query Match 99.4% Score 811: DR 1: Length 157:
 Best Local Similarity 99.4% Pred. No. 1.7e-82:
 Matches 156: Conservative 0 Mismatches 1: Indels 0: Gaps 0:

1 YFKKESKISVFNINQVLFIDGNSPPIFPMITDSCDNNAPRTIFISMYKDSQPRGM 60
 1 YFKKESKISVFNINQVLFIDGNSPPIFPMITDSCDNNAPRTIFISMYKDSQPRGM 60
 61 AVTISVKCKISXLSCKENKISFKENPPNNIKTKSDIFPQSVSPENKMKPFESSSY 120
 61 AVTISVKCKISXLSCKENKISFKENPPNNIKTKSDIFPQSVSPENKMKPFESSSY 120
 121 FQFTVAFKPKGAFITIKKFEETQESIMTVQNEE 157
 121 FQFTVAFKPKGAFITIKKFEETQESIMTVQNEE 157
 121 FQFTVAFKPKGAFITIKKFEETQESIMTVQNEE 157

RESULT 10
 WISCI
 ID WIS701 standard: protein: 157 AA
 AC WIS701:
 DI 26-JAN-1998 (first entry)
 DE Interferon-gamma induced protein:
 KW Interferon-gamma, IFN-gamma, antiviral, antiproliferative, radiotherapy;
 KW immunoregulatory, antitumor agent, chemotherapy, leukopenia;
 KW thymocyte, thymus, immunocompetent cells, asthma; hayfever;
 KW rheumatism, interleukin, killer cell
 OS Homo sapiens
 FH Key
 FT Misc-difference 73
 FT Misc-difference 73 /label= Ile, Thr
 PN EP-767178-A1
 PD 09-APR-1997
 PF 26-SEP-1996: 306997:
 PR 20-SEP-1996: JF-269105:
 PR 25-SEP-1995: JF-270735:
 PR 28-FEB-1994: JP-56734:
 PA HAYASHIBARA SEIBUTSU KAGAKU
 PI Arita K, Fujita M, Furumoto W, Nakada Y, Tanimoto T
 DP WPI: 97-369341/34
 FT Human protein that induces interferon-gamma production in
 PT immunocompetent cells, useful for adoptive immunotherapy of
 PT tumors and as antimicrobial agent etc.
 PS Claim 8: Page 20: 5pp; English.
 CC The present sequence represents a novel protein from human cells, which
 CC induces interferon-gamma (IFN-gamma) production in immunocompetent cells.
 CC This protein enhances cytotoxicity of killer cells and induces their
 CC formation. It is used as an antitumor agent for antitumor
 CC immunotherapy, an antiviral (including anti-AIDS) or antibacterial agent,
 CC and in the treatment of atopic or immune system diseases, e.g. asthma,
 CC hayfever or rheumatism. When formulated with interleukin-3, it is also
 CC used to treat leukopenia and thrombocytopenia associated with
 CC radiotherapy or chemotherapy of leukemia and other cancers. When used in
 CC adjuvant immunotherapy, this novel protein significantly improves the
 CC immunotherapeutic effect of interleukin-2 (IL-2), compared with use of
 CC IL-2 alone, either when administered to the patient (before
 CC administration of IL-2) or by addition to the medium in which cells
 CC (harvested for culture to the patient) are being grown

SU Sequence 157 AA:
 Query Match 99.4% Score 811: DR 1: Length 157:
 Best Local Similarity 99.4% Pred. No. 1.7e-82:
 Matches 156: Conservative 0 Mismatches 1: Indels 0: Gaps 0:

1 YFKKESKISVFNINQVLFIDGNSPPIFPMITDSCDNNAPRTIFISMYKDSQPRGM 60
 1 YFKKESKISVFNINQVLFIDGNSPPIFPMITDSCDNNAPRTIFISMYKDSQPRGM 60
 61 AVTISVKCKISXLSCKENKISFKENPPNNIKTKSDIFPQSVSPENKMKPFESSSY 120
 61 AVTISVKCKISXLSCKENKISFKENPPNNIKTKSDIFPQSVSPENKMKPFESSSY 120
 121 FQFTVAFKPKGAFITIKKFEETQESIMTVQNEE 157
 121 FQFTVAFKPKGAFITIKKFEETQESIMTVQNEE 157
 121 FQFTVAFKPKGAFITIKKFEETQESIMTVQNEE 157

RESULT 11
 W47429
 ID W47429 standard: protein: 193 AA
 AC W47429:
 DI 05-JUN-1998 (first entry)
 DE Interferon-gamma production inducer
 KW Interferon-gamma, IFN-gamma, production inducer, gene therapy;
 KW immunocompetent cells, treatment, prevention, malignant tumour;
 KW viral infection, bacterial infection, immune disease,
 OS Homo sapiens.
 FH Key
 FT Peptide 1-36
 FT Peptide /label= sig-peptide
 FT Peptide 37-193
 FT Peptide /label= mt-peptide
 FT Misc-difference 109
 FT Misc-difference 109 /label= Ile, Thr
 PN EP-816499-A2
 PD 07-JAN-1998
 PF 27-JUN-1997: 304616:
 PR 27-JUN-1996: JF-185305:
 PA (HAY) HAYASHIBARA SEIBUTSU KAGAKU.
 PI Kallimide M, Okura T, Teriige K
 DP WPI: 97-369341/34
 DR N-PSDB: V15825, V15826.
 PT Genetic RNA encoding polypeptide inducing interferon-gamma
 PT production - by immunocompetent cells, useful to treat e.g. human
 PT malignant tumours or viral diseases.
 PS Claim 2: Pages 49-50: 74pp; English.
 CC The present sequence is a protein, which induces
 CC interferon-gamma (IFN-gamma) production in immunocompetent cells.
 CC The protein has high biological activity, including enhancing
 CC cytotoxicity of killer cells and inducing killer cell formation,
 CC in addition to inducing IFN-gamma production by immunocompetent
 CC cells when expressed in mammalian cells, facilitating its use in
 CC low dosages to treat/prevent e.g. malignant tumours, viral or
 CC bacterial infections and immune diseases. As it is expressed in
 CC mammalian cells, it also has low toxicity when used in human
 CC treatments, manifesting side effects. The DNA encoding the protein
 CC can be used in gene therapy, e.g. by injecting vectors containing
 CC the DNA or transplanting cells.
 SO Sequence 193 AA:

Query Match 99.4% Score 811: DR 1: Length 193:
 Best Local Similarity 99.4% Pred. No. 2.2e-82:
 Matches 156: Conservative 0 Mismatches 1: Indels 0: Gaps 0:

1 YFKKESKISVFNINQVLFIDGNSPPIFPMITDSCDNNAPRTIFISMYKDSQPRGM 60
 1 YFKKESKISVFNINQVLFIDGNSPPIFPMITDSCDNNAPRTIFISMYKDSQPRGM 60
 61 AVTISVKCKISXLSCKENKISFKENPPNNIKTKSDIFPQSVSPENKMKPFESSSY 120
 61 AVTISVKCKISXLSCKENKISFKENPPNNIKTKSDIFPQSVSPENKMKPFESSSY 120

CC Immunoprecipitated and as an anti-septic
SO Sequence 157 AA:

Query Match 99.4% Score 811; DB 1; Length 157;
Best Local Similarity 99.4%; Pred. No. 1.7e-82;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFRRFESKISVIRLNQGVLFVQGNPPLEKMTOSTCPNAPPTIFIIISMYSQPRGM 60
DB 1 YFRRFESKISVIRLNQGVLFVQGNPPLEKMTOSTCPNAPPTIFIIISMYSQPRGM 60
QY 61 AVTISVKEKISISCKENKISFEKMPNPNKIKTSKIIFFCRSVPGHDKMKMFESSSY 120
DB 61 AVTISVKEKISISCKENKISFEKMPNPNKIKTSKIIFFCRSVPGHDKMKMFESSSY 120
QY 121 FRRFAEKEKISISCKENKISFEKMPNPNKIKTSKIIFFCRSVPGHDKMKMFESSSY 157
DB 121 FRRFAEKEKISISCKENKISFEKMPNPNKIKTSKIIFFCRSVPGHDKMKMFESSSY 157

RESULT 15

W37740
ID W37740 standard; Protein: 193 AA.
AC W37740:
DI 07-JUL-1998 (first entry)
DE Interferon-gamma inducing precursor peptide.
KW Interferon-gamma inducing precursor peptide; IFN-gamma;
KW Interleukin-1-beta-converting enzyme; ICE; cytotoxicity; killer cell;
KW antiviral agent; antitumour agent; immunopathy agent; antiseptic.
OS Mammalia.
FH Key
FT Protein Location/Qualifiers
FT 36..157 /note="Mature protein"
FT Misc_difference 109
FT 1 /label="Ile, Thr
FT Cleavage_site 36..37
FN EP-821005-A2.
PD 28-JAN-1998.
PE 18-JUL-1997; 305376.
PR 31-JAN-1997; JP-031474.
PR 21-JUL-1996; JP-212167.
PA (HAYB.) HAYASHIBARA SEIICHIRO KAGAKU.
PI Kurimoto M, Tanimoto T;
DR WPI: 98-C08847/05.
DR N-PSDB: V18905.
PI Conversion of interferon-inducing polypeptide precursor to active
PI polypeptide - comprises use of interferon-1-beta-converting enzyme,
PI useful for, e.g., enhancing cytotoxicity by killer cells
PS Claim 2: Pages 14-15; 18pp; English.
CC This is the amino acid sequence for the interferon-gamma (IFN-gamma)
CC inducing precursor peptide, which is cleaved to form the active mature
CC protein when it is in contact with interleukin-1-beta-converting
CC enzyme (ICE). The polypeptide is used for inducing, e.g., production
CC of IFN-gamma a useful biologically active substance, enhancing
CC cytotoxicity by, and inducing the formation of killer cells. The
CC polypeptide may potentially be used as an antiviral, antitumour and
CC immunopathy agent and as an antiseptic.
SO Sequence 193 AA:

Query Match 99.4% Score 811; DB 1; Length 193;
Best Local Similarity 99.4%; Pred. No. 2.2e-82;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFRRFESKISVIRLNQGVLFVQGNPPLEKMTOSTCPNAPPTIFIIISMYSQPRGM 60
DB 1 YFRRFESKISVIRLNQGVLFVQGNPPLEKMTOSTCPNAPPTIFIIISMYSQPRGM 60
QY 61 AVTISVKEKISISCKENKISFEKMPNPNKIKTSKIIFFCRSVPGHDKMKMFESSSY 120
DB 61 AVTISVKEKISISCKENKISFEKMPNPNKIKTSKIIFFCRSVPGHDKMKMFESSSY 120
QY 97 AVTISVKEKISISCKENKISFEKMPNPNKIKTSKIIFFCRSVPGHDKMKMFESSSY 156
DB 97 AVTISVKEKISISCKENKISFEKMPNPNKIKTSKIIFFCRSVPGHDKMKMFESSSY 156

QY 121 FRRFAEKEKISISCKENKISFEKMPNPNKIKTSKIIFFCRSVPGHDKMKMFESSSY 157
DB 121 FRRFAEKEKISISCKENKISFEKMPNPNKIKTSKIIFFCRSVPGHDKMKMFESSSY 157

Search completed: June 23, 1999, 10:56:40
Job time: 79 sec



GenCore version 4.5
Copyright (c) 1993 - 1998 CompuGen Ltd

OM protein : protein search, using sw model

Run on: June 22, 1999, 10:56:40 ; Search time 61.72 seconds

(without alignments) 51.448 Million cell updates/sec

Title: US-09-030-061-7
Perfect score: 812
Sequence: 1 NNGPHTTAVIPNINQVI KKNENCKSVMTLLNHQS 157

Scoring table: BLOSUM62

Searched: 16530 seqs, 4025338 residues

Database: A_Geneseq_34:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Match	Length	DB ID	Description
1	812	100.0	180	W48960	Wild-type mouse Interferon gamma
2	812	100.0	157	W77081	Mouse Interleukin 18
3	806	99.3	157	W77081	Mouse Interleukin 18
4	806	99.3	157	W77081	Mouse Interleukin 18
5	806	99.3	157	W77081	Mouse Interleukin 18
6	806	99.3	157	W77081	Mouse Interleukin 18
7	806	99.3	157	W77081	Mouse Interleukin 18
8	806	99.3	157	W77081	Mouse Interleukin 18
9	806	99.3	157	W77081	Mouse Interleukin 18
10	806	99.3	157	W77081	Mouse Interleukin 18
11	806	99.3	157	W77081	Mouse Interleukin 18
12	806	99.3	157	W77081	Mouse Interleukin 18
13	806	99.3	157	W77081	Mouse Interleukin 18
14	806	99.3	157	W77081	Mouse Interleukin 18
15	806	99.3	157	W77081	Mouse Interleukin 18
16	806	99.3	157	W77081	Mouse Interleukin 18
17	806	99.3	157	W77081	Mouse Interleukin 18
18	806	99.3	157	W77081	Mouse Interleukin 18
19	806	99.3	157	W77081	Mouse Interleukin 18
20	806	99.3	157	W77081	Mouse Interleukin 18
21	806	99.3	157	W77081	Mouse Interleukin 18
22	806	99.3	157	W77081	Mouse Interleukin 18
23	806	99.3	157	W77081	Mouse Interleukin 18
24	806	99.3	157	W77081	Mouse Interleukin 18
25	806	99.3	157	W77081	Mouse Interleukin 18
26	806	99.3	157	W77081	Mouse Interleukin 18
27	806	99.3	157	W77081	Mouse Interleukin 18
28	806	99.3	157	W77081	Mouse Interleukin 18
29	806	99.3	157	W77081	Mouse Interleukin 18
30	806	99.3	157	W77081	Mouse Interleukin 18
31	806	99.3	157	W77081	Mouse Interleukin 18
32	806	99.3	157	W77081	Mouse Interleukin 18
33	806	99.3	157	W77081	Mouse Interleukin 18
34	806	99.3	157	W77081	Mouse Interleukin 18
35	806	99.3	157	W77081	Mouse Interleukin 18
36	806	99.3	157	W77081	Mouse Interleukin 18
37	806	99.3	157	W77081	Mouse Interleukin 18
38	806	99.3	157	W77081	Mouse Interleukin 18
39	806	99.3	157	W77081	Mouse Interleukin 18
40	806	99.3	157	W77081	Mouse Interleukin 18
41	806	99.3	157	W77081	Mouse Interleukin 18
42	806	99.3	157	W77081	Mouse Interleukin 18
43	806	99.3	157	W77081	Mouse Interleukin 18

ALIGNMENTS

44 507 52.4 157 1 W48967 Mutant human Inter
45 507 62.4 157 1 W77081 Human Interleukin

RESULT 1
ID W48960
AC W48960: standard: Peptide: 180 AA.
DE 25-SEP-1998 (first entry)
KW Wild-type mouse interferon-gamma inducing factor:
KW Interferon-gamma inducing factor, interferon-gamma, killer cell:
KW antitumor agent; antiviral agent; antimicrobial agent; tumour MIGF:
KW hepatitis; malaria; tuberculosis; fetal carcinoma; rheumatoid AIDS:
KW osteoporosis; thrombogenic; acquired immunodeficiency syndrome.
OS Mus sp.
FH Key
FT Location/Qualifiers
FT Peptide
FT 1..23
FT /note="Signal peptide"
FT 24..180
FT /note="Mouse IgIF which is claimed by the
FT /note="Inventors under claim 4 in the specification"

EP-845930-A2.
PN 03-JUN-1998.
PD 28-NOV-1997: 309632.
PR 14-NOV-1997: JP-329715.
PR 29-NOV-1996: JP-333037.
PR 21-JAN-1997: JP-029006.
PA (HAYB) HAYASHIBARA SEIBUITSU KAGAKU.
FI Kurimoto M, Okamoto I, Yamamoto K;
FI WFI 38-092737-26.
DE WFSDB: W27255.
FI Mutants of interferon gamma inducing polypeptide used as
FI antitumor, antiviral, antimicrobial or anti immunopathic agents
FI Claim 4, pages 38-39, 59pp, English.
CC The present sequence represents the wild-type mouse interferon gamma
CC inducing factor (MIGF). The invention provides for mutant human and
CC mouse interferon gamma inducing factors in which one or more cysteine
CC residues are replaced with different residues at or away from the
CC positions shown in W48960-W48958. The mutant motifs are
CC capable of stimulating the development of cells for the production of
CC interferon gamma and are claimed to be less toxic, more active and stable
CC than the corresponding wild type MIGF. The mutant motifs are also
CC claimed to enhance killer cell cytotoxicity and/or induce killer cell
CC formation, and may therefore be useful as antitumor agents, antitumor
CC immunotherapeutics, antiviral agents and antimicrobial agents. The
CC mutant motifs are also claimed to be useful for treating hepatitis,
CC acquired immunodeficiency syndrome (AIDS), malaria, tuberculosis, solid
CC malignant tumours (e.g. renal carcinoma), rheumatism, osteoporosis and
CC thromboplasia caused by infection and chemotherapy.
SQ Sequence 180 AA:

Query Match: 100.0% Score 812; DB 1; Length 180
Best Local Similarity: 100.0% Pred. No. 4 16-77
Matches: 111 Conservative 0 Mismatches 0 Gaps 0

QY 1 NNGPHTTAVIPNINQVIFKPPVFEEMITISASIFLLIINYKNSVGLA 60
RQ 24 NNGPHTTAVIPNINQVIFKPPVFEEMITISASIFLLIINYKNSVGLA 63
QY 61 VTFVSGKMSISKNTTFEFEPFENTCSTLFFLVHKNKEEFGYED 129
RQ 64 VTFVSGKMSISKNTTFEFEPFENTCSTLFFLVHKNKEEFGYED 148
QY 121 HFLAQGFEPAPKTTVYFVNSQPSVMTLLNHQS 157
RQ 144 HFLAQGFEPAPKTTVYFVNSQPSVMTLLNHQS 180

RESULT 2

CC carrying the GNA.
S0 Sequence 157 AA

Query Match 99.3% Score 806 DB 1: length 157
Best local similarity 99.4% Prod No 14e-76
Matches 156, Conservative 0, Mismatches 1, Indels 0, Gaps 0

QY 1 NEGRHCTIVAVININQVAVKPKQPVFEDMDIDQASAPETRLIIMYKDSFGLA 60
DB 1 NEGRHCTIVAVININQVAVKPKQPVFEDMDIDQASAPETRLIIMYKDSFGLA 60
QY 61 VITVAVTSEKSTISCKNFIISFEKPKPPNIDICDSELIFFKPPVPGNKKMFESSLEYG 120
DB 61 VITVAVTSEKSTISCKNFIISFEKPKPPNIDICDSELIFFKPPVPGNKKMFESSLEYG 120
QY 121 HFLAQGFRTAFVITLKKKDKNGKSVMTLLNHQS 157
DB 121 HFLAQGFRTAFVITLKKKDKNGKSVMTLLNHQS 157

RESULT 5
W63812
ID W63812 standard; protein: 157 AA.

AC W63812;
DE Mouse protein for induction of interferon-gamma.
KW Interferon-gamma, immunocompetent cells, malignant tumour;
KW viral disease; bacterial infection; immune disease.
OS Mus musculus.

FI misc-difference 70 Location/Qualifiers
FT J09157180-A.
PN 11-JUN-1997
PR 24-JAN-1998 0287222
PR 24-JAN-1998 0287222
PR 10-MAR-1998 0600925
PR 29-SEP-1998 0627499
PA (HAYE / HAYASHIBARA SEINOBU KASAKU,
DB WPI: 97-205381/19.
DR N-PSDB: T60536.
PI A drug containing a polypeptide which induces interferon-gamma -
PI useful for treating e.g. malignant tumours, viral, bacterial or
PI immune diseases.
PS Discovered: Date 10-11-1997, Japanese.
CC This sequence represents a protein which induces interferon-gamma
CC production in immunocompetent cells. This protein may be used as
CC the major component in a drug for the prevention and treatment of
CC e.g. malignant tumours, viral diseases, bacterial infections and
CC immune diseases.
S0 Sequence 157 AA

Query Match 99.3% Score 806 DB 1: length 157
Best local similarity 99.4% Prod No 14e-76
Matches 156, Conservative 0, Mismatches 1, Indels 0, Gaps 0

QY 1 NEGRHCTIVAVININQVAVKPKQPVFEDMDIDQASAPETRLIIMYKDSFGLA 60
DB 1 NEGRHCTIVAVININQVAVKPKQPVFEDMDIDQASAPETRLIIMYKDSFGLA 60
QY 61 VITVAVTSEKSTISCKNFIISFEKPKPPNIDICDSELIFFKPPVPGNKKMFESSLEYG 120
DB 61 VITVAVTSEKSTISCKNFIISFEKPKPPNIDICDSELIFFKPPVPGNKKMFESSLEYG 120
QY 121 HFLAQGFRTAFVITLKKKDKNGKSVMTLLNHQS 157
DB 121 HFLAQGFRTAFVITLKKKDKNGKSVMTLLNHQS 157

RESULT 6
W15704

ID W15704 standard; peptide: 157 AA.

AC W15704;
DE 26-JAN-1998 (first entry)
DE Mouse interferon-gamma inducer protein.
KW Interferon-gamma, IFN-gamma, antiviral; antineoplastic; radiotherapy;
KW immunoregulatory; antitumour agent; chemotherapy; leukaemia;
KW thymocyte; thymus; immunocompetent cells; asthma; hayfever;
KW rheumatism; interleukin; killer cell.
OS Mus musculus.

FI Key Location/Qualifiers
FT misc-difference 70 /label= Met, Thr
FN EF-267178-A1.
PD 09-APR-1997.
PE 24-SEP-1996 305697.
PR 20-SEP-1996 305697.
PR 26-SEP-1996 305697.
PR 29-SEP-1996 305697.
PA (HAYE / HAYASHIBARA SEINOBU KASAKU,
PI Akita K, Fujii M, Kurimoto M, Nukada Y, Tanimoto Y.
DR WPI: 97-205381/19.
DR N-PSDB: T60536.
PI Human protein that induces interferon-gamma prodn. in
PI immuno competent cells - useful for adoptive immunotherapy of
PI tumours and as antimicrobial agent etc.
PS Discovered: Date 22, 2596, English.
CC The present sequence represents a novel protein from mouse liver cells,
CC which induces interferon-gamma (IFN gamma) production in immunocompetent
CC cells. This protein enhances cytotoxicity of killer cells and induces
CC their formation. It is used as an antineoplastic agent for antitumour
CC immunotherapy. An antiviral (including anti-AIDS) or antiparasitic agent,
CC and in the treatment of atopic or immune system diseases, e.g. asthma,
CC hayfever or rheumatism. When formulated with interleukin-3, it is also
CC used to treat leukaemia and thrombocytopenia associated with
CC cytotoxicity of chemotherapy of leukaemia and other cancers. When used
CC in antitumour immunotherapy, this novel protein significantly improves
CC the immunotherapeutic effect of interleukin-2 (IL-2) compared with the
CC administration of IL-2 or by addition to the medium in which cells
CC (harvested for return to the patient) are being grown.
S0 Sequence 157 AA

Query Match 99.3% Score 806 DB 1: length 157
Best local similarity 99.4% Prod No 14e-76
Matches 156, Conservative 0, Mismatches 1, Indels 0, Gaps 0

QY 1 NEGRHCTIVAVININQVAVKPKQPVFEDMDIDQASAPETRLIIMYKDSFGLA 60
DB 1 NEGRHCTIVAVININQVAVKPKQPVFEDMDIDQASAPETRLIIMYKDSFGLA 60
QY 61 VITVAVTSEKSTISCKNFIISFEKPKPPNIDICDSELIFFKPPVPGNKKMFESSLEYG 120
DB 61 VITVAVTSEKSTISCKNFIISFEKPKPPNIDICDSELIFFKPPVPGNKKMFESSLEYG 120
QY 121 HFLAQGFRTAFVITLKKKDKNGKSVMTLLNHQS 157
DB 121 HFLAQGFRTAFVITLKKKDKNGKSVMTLLNHQS 157

RESULT 7

W63811
ID W63811 standard; protein: 157 AA.
AC W63811;
DE 28-SEP-1998 (first entry)
DE Mouse IL-18 protein fragment.
KW Interleukin-18, IL-18, murine; treatment; autoimmune disease; antibody;
KW immunosuppressant; inhibitor; receptor protein; detection.
OS Mus sp.
FI Key Location/Qualifiers
FT 1..157 /label= IL-18
FT Protein
FT /note= "partial sequence"

CC mutant human and mouse interferon-gamma inducing factors in which one
CC or more of the positions are replaced with different residues at or away
CC from the consensus sequence shown in W4896-W4898. The mutant MIGFs
CC are capable of stimulating immunocompetent cells for the production of
CC interferon-gamma and are claimed to be less toxic, more active and stable
CC than the corresponding wild type MIGF. The mutant MIGFs are also
CC claimed to enhance killer cell cytotoxicity and/or induce killer cell
CC formation and may therefore be useful as antitumour agents, antitumour
CC immunotherapeutics, antiviral agents and antimicrobial agents. The
CC mutant MIGFs are also claimed to be useful for treating hepatitis,
CC acquired immunodeficiency syndrome (AIDS), malaria, tuberculosis, solid
CC malignant tumours (e.g. renal carcinoma), rheumatism, osteoporosis and
CC thrombocytopenia caused by radiation and chemotherapy.

SO Sequence 157 AA;

Query Match 99.9% Score 803 DB 1 Length 157

Best Local Similarity 99.4% Prod. No. 2.9e-76;

Matches 156, Conservative 0, Mismatches 1, Indels 0, Gaps 0;

QY 1 NFGHNTAVINININAVIIVKQVPEVEMTRIDQASSEPCTPLIIMKDSVAGLA 60
DB 1 NFGHNTAVINININAVIIVKQVPEVEMTRIDQASSEPCTPLIIMKDSVAGLA 60
QY 61 VTSVTSKSWKSTLSPNNTISEEMEPENITDLSLAFKRPVQHKKEFESSLEYS 120
DB 61 VTSVTSKSWKSTLSPNNTISEEMEPENITDLSLAFKRPVQHKKEFESSLEYS 120
QY 121 HFLAALAKRFAVETIKRKEFNQKSVKGLINLHQSS 157
DB 121 HFLAALAKRFAVETIKRKEFNQKSVKGLINLHQSS 157

RESULT 10

W77090
ID W77090 standard, Peptide, 157 AA.

AC W77090;

DT 16-NOV-1998 (first entry)

DE Mouse Interleukin 18 derivative 1.

KW Mouse Interleukin 18, IL18, osteoclast, hypercalcaemia, osteopenia,

KN osteoclastoma, Behcet's syndrome, osteosarcoma, archagopathy, osteoporosis,

OS Osteoclastoma, Behcet's syndrome, osteosarcoma, archagopathy, osteoporosis,

Mus sp.

PN EP-861663-A2;

PD 02-SEP-1998;

PF 24-SEP-1998; 201872

PR 25-SEP-1998; 201872

PA (HAI18) HAYASHIBARA SEIICHIRO KAGAKU,

PI Gill, Leslie M; Hattori, M; Kuriyama, M; Nagawa, N

DR WPI/98-44864/39;

PT Use of Interleukin 18 to inhibit osteoclast formation in treatment

of osteoclastoma, Behcet's syndrome, osteosarcoma, archagopathy,

PI osteoclastoma, Behcet's syndrome, osteosarcoma, archagopathy,

PS Primary hyperparathyroidism and osteoporosis

CC Interleukin-18 (IL-18) or a functional equivalent can be used for

CC inhibition of osteoclast formation. IL-18 is used for treating or

CC preventing osteoclast-related diseases e.g. hypercalcaemia, osteoporosis,

CC Behcet's syndrome, osteosarcoma, archagopathy, chronic rheumatoid

CC arthritis, deformity, osteitis, primary hyperthyroidism, osteopenia and

CC osteoporosis.

SO Sequence 157 AA;

Query Match 99.9% Score 803 DB 1 Length 157
Best Local Similarity 99.4% Prod. No. 2.9e-76;
Matches 156, Conservative 0, Mismatches 1, Indels 0, Gaps 0;

QY 1 NFGHNTAVINININAVIIVKQVPEVEMTRIDQASSEPCTPLIIMKDSVAGLA 60
DB 1 NFGHNTAVINININAVIIVKQVPEVEMTRIDQASSEPCTPLIIMKDSVAGLA 60

QY 61 VTSVTSKSWKSTLSPNNTISEEMEPENITDLSLAFKRPVQHKKEFESSLEYS 120
DB 61 VTSVTSKSWKSTLSPNNTISEEMEPENITDLSLAFKRPVQHKKEFESSLEYS 120
QY 121 HFLAALAKRFAVETIKRKEFNQKSVKGLINLHQSS 157
DB 121 HFLAALAKRFAVETIKRKEFNQKSVKGLINLHQSS 157

RESULT 11

W48969

ID W48969 standard, Peptide, 157 AA.

AC W48969;

DT 05-SEP-1998 (first entry)

DE Mutant mouse interferon-gamma inducing factor mIGF/MIG12.

KW Interferon-gamma inducing factor; Interferon-gamma; Killer cell;

KW antitumour agent; antiviral agent; antimicrobial agent; tumour; MIGF;

KW hepatitis, malaria, tuberculosis, renal carcinoma, rheumatism, AIDS;

KW osteoporosis, thrombocytopenia, acquired immunodeficiency syndrome,

OS Mus sp.

PN Synthetic.

PF Key location/Qualifiers

FT MISC: difference 125

FT /score: replaced from 275 to wild type to get in

FT mutant

FT

FN EF-845930-A2;

PD 03-JUN-1998;

PE 08-NOV-1997; 409632;

PR 14-NOV-1997; JP-329715;

PS 29-NOV-1997; JP-323037;

PT 21-JAN-1997; JP-020906;

PA (HAYE) HAYASHIBARA SEIICHIRO KAGAKU,

PI Kuriyama, M; Okamoto, T; Yamamoto, K;

DR WPI/98-288747/26;

DT N-PSDB; V32633;

PT Mutants of interferon-gamma inducing polypeptide useful as

PI antitumour, antiviral, antimicrobial or anti-immunoproliferative

PS claim 5; page 44; 59pp; English.

CC The present sequence represents the mutant mouse interferon-gamma

CC inducing factor mIGF/MIG12. The wild-type mouse interferon-gamma

CC factor (wild) sequence is shown in W48969. The invention provides for

CC mutant human and mouse interferon-gamma inducing factors in which one

CC or more cysteine residues are replaced with different residues at or away

CC from the consensus sequence shown in W48969-W4898. The mutant MIGFs

CC are capable of stimulating immunocompetent cells for the production of

CC interferon-gamma and are claimed to be less toxic, more active and stable

CC than the corresponding wild type MIGF. The mutant MIGFs are also

CC claimed to enhance killer cell cytotoxicity and/or induce killer cell

CC formation, and may therefore be useful as antitumour agents, antitumour

CC immunotherapeutics, antiviral agents and antimicrobial agents. The

CC mutant MIGFs are also claimed to be useful for treating hepatitis,

CC acquired immunodeficiency syndrome (AIDS), malaria, tuberculosis, solid

CC malignant tumours (e.g. renal carcinoma), rheumatism, osteoporosis and

CC thrombocytopenia caused by radiation and chemotherapy.

SO Sequence 157 AA;

Query Match 99.9% Score 803 DB 1 Length 157

Best Local Similarity 99.4% Prod. No. 2.9e-76;

Matches 156, Conservative 0, Mismatches 1, Indels 0, Gaps 0;

QY 1 NFGHNTAVINININAVIIVKQVPEVEMTRIDQASSEPCTPLIIMKDSVAGLA 60
DB 1 NFGHNTAVINININAVIIVKQVPEVEMTRIDQASSEPCTPLIIMKDSVAGLA 60
QY 61 VTSVTSKSWKSTLSPNNTISEEMEPENITDLSLAFKRPVQHKKEFESSLEYS 120
DB 61 VTSVTSKSWKSTLSPNNTISEEMEPENITDLSLAFKRPVQHKKEFESSLEYS 120
QY 121 HFLAALAKRFAVETIKRKEFNQKSVKGLINLHQSS 157
DB 121 HFLAALAKRFAVETIKRKEFNQKSVKGLINLHQSS 157

DB 138 GHFLACQCKEDPAFLVLRKXNDGCKSVMTLLNLKQS 175

RESULT 15

ID W48962 standard: Peptide: 157 AA.

AC W48962:

DI 25-SEP-1998 (first entry)

DE Mutant human interferon gamma inducing factor IGIF/MOT21.

KW Interferon-gamma inducing factor, interferon-gamma, killer cell,

KW Antitumor agent; antimicrobial agent; tumour; IGIF;

KW hepatitis; malaria; tuberculosis; renal carcinoma; rheumatism; AIDS;

KW Osteoporosis, thrombocytosis, acquired immunodeficiency syndrome.

OS Homo sapiens.

OS Synthetic.

EH Key Location/Qualifiers

FI MISC_difference 38 /note= "changed from Cys in wild-type to Ser in

FI mutant"

PI EP-845530-A2.

PD 03-JUN-1998.

PE 20-NOV-1998: 309622.

PR 14-NOV-1997: JP-329715.

PR 29-NOV-1996: JP-333037.

PR 21-JAN-1997: JP-020904.

PA (HAYB.) HAYASHIWARA SEIJIHISU KAGAKU.

PI KURIMOTO M, OKAMOTO I, YAMAMOTO K;

DR WPI: 98-286747/25.

DR N-PSDB: V32626.

PI Mutants of interferon-gamma inducing polypeptide - useful as

PI antitumor, antiviral, antimicrobial or anti immunopathic agents

PS Claim 5: page 41: 59pp: English.

CC The present sequence represents the mutant human interferon-gamma

CC inducing factor IGIF/MOT21. The wild-type human interferon-gamma

CC factor sequence is shown in W48959. The invention provides for mutant

CC human and mouse interferon-gamma inducing factors (IGIF) in which one or

CC more cysteine residues are replaced with different residues at or away

CC from the consensus sequences shown in W48956-W48958. The mutant IGIFs

CC are capable of stimulating immunocompetent cells for the production of

CC interferon-gamma and are claimed to be less toxic, more active and

CC stable than the corresponding wild type interferon-gamma inducing

CC factor. The mutant IGIFs are also claimed to enhance killer cell

CC cytotoxicity and/or induce killer cell formation, and may therefore

CC be useful as antitumor agents, antitumor immunotherapeutics, antiviral

CC agents and antimicrobial agents. The mutant IGIFs are also claimed

CC to be useful for treating hepatitis, acquired immunodeficiency syndrome

CC (AIDS), malaria, tuberculosis, solid malignant tumours (e.g. renal

CC carcinoma), rheumatism, osteoporosis and thrombocytopenia caused by

CC radiation and chemo-therapy.

SO Sequence: 157 AA;

Query Match 64.8%, Score 526, DB 1, Length 157,

Best Local Similarity 65.6%; Pred. No. 1.7e-47;

Matches 191; Conservation 27; Mismatches 24; Indels 2; Gaps 2;

Q3 2 EGRHCTAVININQGVFEVK-EGVEFEDMDITQASSEPTRLIIYMKSEVGLA 60

DB 2 FQTFKTLVIANINQGVFEVK-EGVEFEDMDITQASSEPTRLIIYMKSEVGLA 61

QY 61 VILSVKSKAKTISQNNKLTSEEMUPENIDIDQSLDFEQPVPGH-NKKEFESSIVE 119

DB 62 VILSVKSKAKTISQNNKLTSEEMUPENIDIDQSLDFEQPVPGH-NKKEFESSIVE 119

Q3 123 GHFLACQCKEDPAFLVLRKXNDGCKSVMTLLNLKQS 175

DB 122 GHFLACQCKEDPAFLVLRKXNDGCKSVMTLLNLKQS 175



GenCore version 4.5
Copyright 1993-1998 Amgen Inc.

OM protein - protein search, using SW model

Run on: June 22, 1999, 10:55:21 ; Search time 61.72 seconds

(without alignments)
1.966 Million cell updates/sec

Title: US-09-030-061-1

Perfect score: 31

Sequence: 1 NDVLF 6

Scoring table: PROSUM62

Search: 11899 943 2029728 residues

Database: A_Geneseq_34:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	157	1	R92506 Interferon gamma F
2	31	100.0	157	1	R92506 Human interferon-g
3	31	100.0	157	1	R94858 Human mature inter
4	31	100.0	157	1	R94859 Mouse mature inter
5	31	100.0	157	1	R94860 Human interferon-g
6	31	100.0	157	1	R94861 Human interferon-g
7	31	100.0	157	1	R94862 Human protein for
8	31	100.0	157	1	R94863 Human protein for
9	31	100.0	157	1	R94864 Human protein for
10	31	100.0	157	1	R94865 Human protein for
11	31	100.0	157	1	R94866 Human protein for
12	31	100.0	157	1	R94867 Human protein for
13	31	100.0	157	1	R94868 Human protein for
14	31	100.0	157	1	R94869 Human protein for
15	31	100.0	157	1	R94870 Human protein for
16	31	100.0	157	1	R94871 Human protein for
17	31	100.0	157	1	R94872 Human protein for
18	31	100.0	157	1	R94873 Human protein for
19	31	100.0	157	1	R94874 Human protein for
20	31	100.0	157	1	R94875 Human protein for
21	31	100.0	157	1	R94876 Human protein for
22	31	100.0	157	1	R94877 Human protein for
23	31	100.0	157	1	R94878 Human protein for
24	31	100.0	157	1	R94879 Human protein for
25	31	100.0	157	1	R94880 Human protein for
26	31	100.0	157	1	R94881 Human protein for
27	31	100.0	157	1	R94882 Human protein for
28	31	100.0	157	1	R94883 Human protein for
29	31	100.0	157	1	R94884 Human protein for
30	31	100.0	157	1	R94885 Human protein for
31	31	100.0	157	1	R94886 Human protein for
32	31	100.0	157	1	R94887 Human protein for
33	31	100.0	157	1	R94888 Human protein for
34	31	100.0	157	1	R94889 Human protein for
35	31	100.0	157	1	R94890 Human protein for
36	31	100.0	157	1	R94891 Human protein for
37	31	100.0	157	1	R94892 Human protein for
38	31	100.0	157	1	R94893 Human protein for
39	31	100.0	157	1	R94894 Human protein for
40	31	100.0	157	1	R94895 Human protein for
41	31	100.0	157	1	R94896 Human protein for
42	31	100.0	157	1	R94897 Human protein for
43	31	100.0	157	1	R94898 Human protein for

44 31 100.0 157 1 W77087 Human Interleukin
45 31 100.0 157 1 W77088 Human Interleukin

ALIGNMENTS

RESULT 1
R92506
ID R92506 standard: Protein: 157 AA.
AC R92506;
DE 02-SEP-1996 (first entry)
DE Interferon gamma production inducer protein.
KW Interferon gamma inducer IFNgamma (amino-acid-seq) (sol) (antibody)
KW antitumor; antiseptic; immunoregulatory; platelet increasing agent;
KW therapeutic; cytotoxic; cytostatic; cytoreductive; platelet cancer; platelet cancer;
KW 9101-1994; myeloid leukemia; thrombocytopenia; platelet cancer; platelet cancer;
KW 9101-1994; myeloid leukemia; thrombocytopenia; platelet cancer; platelet cancer;
KW 9101-1994; myeloid leukemia; thrombocytopenia; platelet cancer; platelet cancer;
KW adoptive immunotherapy; monoclonal antibody.
OS Mus musculus.
FR key Location/Qualifiers
HI misc_difference /0
IN 17-JAN-1996.
PD 13-JUL-1995: 304906.
PR 14-JUL-1994: JP-184162.
PR 10-FEB-1995: JP-045057.
FA (HMB) HAYASHIBARA SEIBUICHI KASAKU;
PI Kohno K, Kunikida T, Kurimoto M, Okamura H, Taniguchi M;
PI Tanimoto T, Toriige K;
PI WPI: 96-070177/08.
NP N-PSDB: 192506.
PT Protein that induces gamma interferon prodn. in immunocompetent
PI cells - used e.g. as activator or antitumor agent, also induces
PI cytotoxicity of killer cells.
FS Claim 2, Page 22, 30PP, English.
CC This sequence represents the interferon gamma (IFNgamma) inducer protein
CC of the invention. This protein induces IFNgamma production in
CC immunocompetent cells. The protein is useful as an antiviral,
CC antitumor, anti-prion, immunoregulatory and platelet-increasing agent.
CC It can be used for treatment or prevention AIDS, Kaposi's sarcoma, and
CC other viral cancer, granuloma, myeloid leukemia, thrombocytopenia and
CC allergy. The protein can also be used to induce IFNgamma production in
CC cultured cells. The IFNgamma inducer strongly induces cytotoxicity of
CC killer T cells and when used with interleukin-2 (IL-2) and tumor
CC necrosis factor (TNF), may improve the effect (or reduce side effects) of
CC adoptive immunotherapy in humans. The DNA encoding this sequence can
CC be used to produce the protein, which can then be purified for assay
CC using monoclonal antibodies.
SO Sequence 157 AA;

Query Match 100.0% Score 31; DB 1; Length 157;
Best local similarity 100.0%, P003; No 2.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QV 1 NDVLF 6
|||||
DB 16 NDVLF 21

RESULT 2
R99564
ID R99564 standard: Protein: 157 AA.
AC R99564;
DE 29-SEP-1996 (first entry)
DE Human interferon gamma inducer protein.
KW Interferon-gamma inducer protein; IFN-gamma; antitumor; cytotoxic;
KW antitumor; cytotoxic; cytostatic; cytoreductive; platelet cancer;
KW 9101-1994; myeloid leukemia; thrombocytopenia; platelet cancer; platelet cancer;
KW 9101-1994; myeloid leukemia; thrombocytopenia; platelet cancer; platelet cancer;
KW adoptive immunotherapy; monoclonal antibody.
OS Homo sapiens.
FR key Location/Qualifiers

DE Human interferon gamma inducer protein.
 KW Interferon gamma inducer protein, IFN-gamma, antiviral, virucide,
 KW antitumor, antibacterial, immunomodulator, antiviral immunotherapy.
 KW therapy, cancer.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT peptide 1..36
 FT /label= Leader-peptide
 FT protein 37..193
 FT /label= Mat-protein
 FT misc_difference 109
 FT /label= ILE, ILE
 PN EP-312931-A2
 PD 22-MAY-1996
 PE 10-NOV-1995
 PR 15-NOV-1994 JP-304203
 PR 23-FEB-1995 JP-058240
 PR 10-MAR-1995 JP-078357
 PR 18-SEP-1995 JP-262062
 PR 29-SEP-1995 JP-274988
 PA (HAYR.) HAYASHIHARA SEIBOTSU KAKAKU.
 PI Fukuoka S. Kaku K. Kunitada T. Kunitada M. Okamura H.
 PI Taniguchi M. Taniguchi T. Torioka K. Ushio S.
 DI WJ24258 standard; Protein: 157 AA.
 DR N-PSDB:182020.
 PI DNA encoding interferon gamma protein-inducing polypeptide - useful
 PI to treat and prevent viral disease, malignancies and immune
 PI disorders.
 PS Claim 6: Page 41-42: 48pp; English.
 CC The amino acid sequence of a novel human protein (P06660) induces
 CC interferon-gamma (IFN-gamma) production by immunocompetent cells. It
 CC is the product of a cDNA clone (132404) cld. from a human liver
 CC library. The protein enhances the cytotoxicity of killer cells
 CC and/or induces the formation of killer cells (e.g. NK cells,
 CC lymphokine-activated killer (LAK) cells, and cytotoxic T-cells).
 CC The mature protein (see also P06660) is useful as an antiviral,
 CC antitumor, antibacterial, immunoregulatory and blood platelet
 CC enhancing agent and can be used in adoptive immunotherapy. It is
 CC also used in passive immunization and antibodies.
 SO Sequence 193 AA.
 Query Match 100.0%; Score 31; E 1 Length 193;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 NC0416 6
 DB 52 NOVLEF 57
 RESULT 6
 W24252
 ID W24252 standard; Protein: 157 AA.
 AC W24252
 DI 15-OCT-1997 (first entry)
 DE Mature protein for induction of interferon-gamma.
 KW Interferon gamma; immunocompetent cell; malignant tumour;
 KW viral disease; bacterial infection; immune disease.
 OS Mus musculus.
 FH Key Location/Qualifiers
 FT misc_difference 70
 FT /note= "Encoded by AYR"
 PN J09157180-A.
 PD 17-JUN-1997
 PE 21-JAN-1996
 PR 04-OCT-1995 JP-279906
 PR 10-MAR-1995 JP-078357
 PR 29-SEP-1995 JP-274988
 PA (HAYR.) HAYASHIHARA SEIBOTSU KAKAKU
 PI WPI: 97-36931/31.
 DR N-PSDB:182020.
 PT A drug containing a polypeptide which induces interferon gamma -

PT useful for treating a malignant tumour, viral, bacterial or
 IT immune diseases.
 IS Disclosure: Page 10-11, 12ff, Japanese.
 CC This sequence represents a protein which induces interferon-gamma
 CC production in immunocompetent cells. This protein may be used as
 CC the major component in a drug for the prevention and treatment of
 CC a malignant tumour, viral diseases, bacterial infections and
 CC immune diseases.
 SO Sequence 157 AA;
 Query Match 100.0%; Score 31; DB 1; Length 157;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 NOVLEF 6
 DB 16 NOVLEF 21
 RESULT 7
 W24258
 ID W24258 standard; Protein: 157 AA.
 AC W24258
 DI 15-OCT-1997 (first entry)
 DE Human protein for induction of interferon-gamma.
 KW Interferon-gamma, immunocompetent cell; malignant tumour;
 KW viral disease; bacterial infection; immune disease.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT misc_difference 73
 FT /note= "Encoded by AYR"
 PN J09157180-A.
 PD 17-JUN-1997
 PE 21-JAN-1996
 PR 04-OCT-1995 JP-279906
 PR 10-MAR-1995 JP-078357
 PR 29-SEP-1995 JP-274988
 PA (HAYR.) HAYASHIHARA SEIBOTSU KAKAKU.
 PI WPI: 97-36931/31.
 DR N-PSDB:182020.
 PI A drug containing a polypeptide which induces interferon gamma -
 PI useful for treating a malignant tumour, viral, bacterial or
 PI immune diseases.
 PS Claim 6: Page 9, 12ff; Japanese.
 CC This sequence represents a protein which induces interferon-gamma
 CC production in immunocompetent cells. This protein may be used as
 CC the major component in a drug for the prevention and treatment of
 CC a malignant tumour, viral diseases, bacterial infections and
 CC immune diseases.
 SO Sequence 157 AA;
 Query Match 100.0%; Score 31; DB 1; Length 157;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 NOVLEF 6
 DB 16 NOVLEF 21
 RESULT 8
 W31757
 ID W31757 standard; Protein: 193 AA.
 AC W31757
 DI 15-JAN-1998 (first entry)
 DE Interferon gamma inducing factor-2 (IGIF-2) R1401 variant.
 KW Interferon gamma inducing factor 2, IGIF-2, leukocyte, lymphocyte, human
 KW inflammation; proliferation; differentiation; maturation; tissue damage.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT misc_difference 140

10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510
 511
 512
 513
 514
 515
 516
 517
 518
 519
 520
 521
 522
 523
 524
 525
 526
 527
 528
 529
 530
 531
 532

CC or treat IGIF-2 induction of proliferation, differentiation of maturation
CC of leukocytes of lymphocytes, especially in patients with disease
CC associated with inflammation.
SO Sequence 193 AA:

Query Match 100.0% Score 31: DB 1: Length 193
Best Local Similarity 100.0%: Pred. No. 3.2:
Matches 5: Conservative 0: Mismatches 0: Indels 0: Gaps

OY 1 NDQVLF 6
|||||
DB 52 NDQVLF 57

RESULT 10
W15704
W15704 standard: peptide: 157 AA.

AC W15704
ID 26-JAN-1998 (first entry)
DE Mouse interferon gamma inducer protein.
KW Interferon-gamma, IFN-gamma, antiviral, antitumor, antiproliferative, radiotherapy,
KW immunoregulatory, antitumor agent, immunomodulator, antiproliferative, antiproliferative,
KW chromocytoma, immunocompetent cell, asthma, hay fever,
KW rheumatism, interleukin, killer cell,
OS Mus musculus.
PM Key: Interferon/Gamma/Inducers
PT Misc. Difference 70 /label= Met, Thr
PI EP 767178-A1.
PD 09-APR-1997.
PF 26-SEP-1996: JP-269105.
PR 20-SEP-1996: JP-269105.
PR 26-SEP-1995: JP-270725.
PR 29-FEB-1996: JP-067434.
PA (HAYE) HAYASHIMAWA SHIGERU KAGAKU.
PI Akita K, Fujii M, Kurimoto M, Nakada Y, Tanimoto T;
WP: 97/205381/19.
DR N-PSDB; 160536.
PT Human protein that induces interferon-gamma prodn. It
PI immunocompetent cells - useful for adoptive immunotherapy of
PI tumours and as antimicrobial agent etc.
PS Disclosure: Page 23: 26pp; English.

CC The present sequence represents a novel protein from mouse liver cells,
CC which induces interferon gamma (IFN gamma) production in immunocompetent
CC cells. This protein enhances cytotoxicity of killer cells and induces
CC their formation. It is used as an antiproliferative agent for antitumor
CC immunotherapy, an antiviral (including anti-AIDS) or antibacterial agent,
CC and in the treatment of allergic or immune system diseases, e.g. asthma,
CC hay fever or rheumatism. When formulated with interleukin-3, it is also
CC used to treat leukopenia and thrombocytopaenia associated with
CC radiotherapy or chemotherapy of leukemia and other cancers. When used
CC in antitumor immunotherapy, this novel protein synergistically improves
CC the immunotherapeutic effect of interleukin-2 (IL-2), compared with use
CC of IL-2 alone, either when administered to the patient (before
CC administration of IL-2) or by addition to the medium in which cells
CC (intended for return to the patient) are being grown.

SO Sequence 157 AA:

Query Match 100.0% Score 31: DB 1: Length 157
Best Local Similarity 100.0%: Pred. No. 2.5:
Matches 5: Conservative 0: Mismatches 0: Indels 0: Gaps

OY 1 NDQVLF 6
|||||
DB 16 NDQVLF 21

RESULT 11
W15697
W15697 standard: peptide: 50 AA.
ID W15697:
AC W15697:

Downloaded from <http://ajphaphysocpharm.sagepub.com/> at 11:06 11 November 2014

Accession: A27174
 Protein: 61, 650 (654), 1987
 A:Title: MAPI and nucleotide sequence of the vaccinia virus gene that encodes a 14-kDa
 A:Accession: A27174; MIMD:88036210
 A:Keywords: A27174
 A:Molecule type: DNA
 A:Position: 1110 (100)
 A:Cross-references: 38;M18174; NID:q335628; PID:q335629
 A:Notes: The authors translated the codon GGA for residue 8 as Lys and AAT for residue 43
 correspondingly. Vaccinia virus 14k cell fusion protein
 A:Keywords: glycoprotein membrane fusion
 A:2-136/Product: 14k cell fusion protein #status predicted <MAT>
 A:Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 90.3% Score 28; DB 1; Length 110;
 Best Local Similarity 83.3% Pred. No. 6;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 NDCVLF 6
 111111
 NDEVLF 6
 111111
 A:Title: MAPI and nucleotide sequence of the vaccinia virus gene that encodes a 14-kDa
 A:Accession: A27174; MIMD:88036210
 A:Keywords: A27174
 A:Molecule type: DNA
 A:Position: 1110 (100)
 A:Cross-references: 38;M18174; NID:q335628; PID:q335629
 A:Notes: The authors translated the codon GGA for residue 8 as Lys and AAT for residue 43
 correspondingly. Vaccinia virus 14k cell fusion protein
 A:Keywords: glycoprotein membrane fusion
 A:2-136/Product: 14k cell fusion protein #status predicted <MAT>
 A:Binding site: carbohydrate (Asn) (covalent) #status predicted

Accession: A27174
 Protein: 61, 650 (654), 1987
 A:Title: MAPI and nucleotide sequence of the vaccinia virus gene that encodes a 14-kDa
 A:Accession: A27174; MIMD:88036210
 A:Keywords: A27174
 A:Molecule type: DNA
 A:Position: 1110 (100)
 A:Cross-references: 38;M18174; NID:q335628; PID:q335629
 A:Notes: The authors translated the codon GGA for residue 8 as Lys and AAT for residue 43
 correspondingly. Vaccinia virus 14k cell fusion protein
 A:Keywords: glycoprotein membrane fusion
 A:2-136/Product: 14k cell fusion protein #status predicted <MAT>
 A:Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 90.3% Score 28; DB 1; Length 110;
 Best Local Similarity 83.3% Pred. No. 6;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

A:Accession: A37076
 A:Molecule type: DNA
 A:Position: 1116 (100)
 A:Cross-references: EMBL:M37086; NID:q335300; PID:q335301
 A:Superfamily: vaccinia virus 14k cell fusion protein
 A:Keywords: glycoprotein membrane fusion
 A:2-136/Product: 14k cell fusion protein #status predicted <MAT>
 A:Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 90.3% Score 28; DB 1; Length 136;
 Best Local Similarity 83.3% Pred. No. 7.6;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 NDCVLF 6
 111111
 NDEVLF 6
 101 NDEVLF 106

RESULT 6
 C64438
 Phenylalanine--tRNA ligase (EC 6.1.1.20) beta chain - Methanococcus jannaschii
 N:Alternate names: phenylalanyl-tRNA synthetase, subunit beta
 C:Species: Methanococcus jannaschii
 C>Date: 13-Sep-1996 #sequence, revision 13-Sep-1996 #text, latest 21-Aug-1997
 C:Accession: C64438
 R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, J.D.; Plak
 erson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hunkeler, M.A.; Raine
 Science 273, 1058-1073, 1995
 A:Authors: Borodovsky, M.; Klock, H.F.; Fraser, C.M.; Smith, H.O.; Woese, C.R.; Venter
 A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
 A:Reference number: A64300; MIMD:6637999
 A:Accession: C64438
 A:Status: Preliminary; nucleotide sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-548 <BUT>
 A:Cross-references: CB:067553, GB:U77117; NID:q1591744; PID:q1591750; PID:M1118; PI
 A:Map position: PEV104809,194712
 C:Superfamily: yeast cytosolic phenylalanine-tRNA ligase, protein biosynthesis
 C:Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 90.3% Score 28; DB 2; Length 548;
 Best Local Similarity 83.3% Pred. No. 37;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 NDCVLF 6
 111111
 NDEVLF 395

RESULT 7
 A41029
 integrin beta-8 chain precursor - human
 C:Species: Homo sapiens (man)
 C>Date: 30-Jun-1992 #sequence, revision 30-Jun-1992 #text, latest 06-Sep-1997
 C:Accession: A41029
 R:Moyle, M.; Napier, M.A.; McLean, J.W.
 J. Biol. Chem. 266, 19650-19658, 1991
 A:Title: Cloning and expression of a divergent integrin subunit beta-8.
 A:Reference number: A41029; MIMD:92011767
 A:Accession: A41029
 A:Molecule type: mRNA
 A:Residues: 1-769 <MOV>
 A:Cross-references: GR:M73780; NID:q14520; PID:q14521
 C:Superfamily: integrin beta chain
 C:Keywords: cell adhesion; cytoskeleton; duplication; extracellular matrix; glycoprotein

Query Match 90.3% Score 28; DB 2; Length 769;
 Best Local Similarity 83.3% Pred. No. 54;

Matches 5: Conservative 1: Mismatches 0: Indels 0: Gaps 0:
QY 1 NDQVLF 6
11:111
Db 425 NDEVLF 430

RESULT 8
S29911

hypothetical protein 5 - vaccinia virus

C:Species: vaccinia virus

C>Date: 06-Jan-1995 #sequence_revision 20-Feb-1995 #text_change 08-Sep-1997

C:Accession: S29911

R:Amegadze, B.Y.

submitted to the EMBL Data Library, January 1991

A:Reference number: S29907

A:Accession: S29911

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1110 <MEV>

A:Cross-references: EMBL:X75156, NID:9404278, PDB:5404274

C:Superfamily: vaccinia virus 14k cell fusion protein

Query Match 90.3% Score 28; DB 2; Length 110;
Best Local Similarity 83.3% Pred. No. 6;
Matches 5: Conservative 1: Mismatches 0: Indels 0: Gaps 0:

QY 1 NDQVLF 6
11:111
Db 75 NDEVLF 80

RESULT 9
S37292

fusion protein, 14k - ectromelia virus

C:Species: Ectromelia virus

C>Date: 06-Jan-1995 #sequence_revision 26-May-1995 #text_change 08-Sep-1997

C:Accession: S37292

R:Krieger, H.; Osterrieder, X.Y.Z.; Gorny, X.Y.Z.

submitted to the EMBL Data Library, September 1993

A:Description: Identification of binding sites for neutralizing mabs.

A:Reference number: S37274

A:Accession: S37282

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1110 <MEV>

A:Cross-references: EMBL:X75157, NID:9404280, PDB:5404281

A:Note: The fusion is designated as monkeypox virus

C:Superfamily: vaccinia virus 14k cell fusion protein

Query Match 90.3% Score 28; DB 2; Length 110;
Best Local Similarity 83.3% Pred. No. 6;
Matches 5: Conservative 1: Mismatches 0: Indels 0: Gaps 0:

QY 1 NDQVLF 6
11:111
Db 75 NDEVLF 80

RESULT 10
S37281

fusion protein, 14k - monkeypox virus

C:Species: monkeypox virus

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Sep-1997

C:Accession: S37281

R:Krieger, H.; Osterrieder, X.Y.Z.; Gorny, X.Y.Z.

submitted to the EMBL Data Library, September 1993

A:Description: Identification of binding sites for neutralizing mabs.

A:Reference number: S37274

A:Accession: S37281

A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1110 <MEV>
A:Cross-references: EMBL:X75156, NID:9404278, PDB:5404279
C:Superfamily: vaccinia virus 14k cell fusion protein

Query Match 90.3% Score 28; DB 2; Length 110;
Best Local Similarity 83.3% Pred. No. 6;
Matches 5: Conservative 1: Mismatches 0: Indels 0: Gaps 0:

QY 1 NDQVLF 6
11:111
Db 75 NDEVLF 80

RESULT 11
S37275

fusion protein, 14k - cowpox virus

C:Species: cowpox virus

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Sep-1997

C:Accession: S37275

R:Krieger, H.; Osterrieder, X.Y.Z.; Gorny, X.Y.Z.

submitted to the EMBL Data Library, September 1993

A:Description: Identification of binding sites for neutralizing mabs.

A:Reference number: S37274

A:Accession: S37275

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1110 <MEV>

A:Cross-references: EMBL:X75156, NID:9404280, PDB:5404284

C:Superfamily: vaccinia virus 14k cell fusion protein

Query Match 90.3% Score 28; DB 2; Length 110;
Best Local Similarity 83.3% Pred. No. 6;
Matches 5: Conservative 1: Mismatches 0: Indels 0: Gaps 0:

QY 1 NDQVLF 6
11:111
Db 75 NDEVLF 80

RESULT 12
S37274

fusion protein, 14k - camelpox virus

C:Species: camelpox virus

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Sep-1997

C:Accession: S37274

R:Krieger, H.; Osterrieder, X.Y.Z.; Gorny, X.Y.Z.

submitted to the EMBL Data Library, September 1993

A:Description: Identification of binding sites for neutralizing mabs.

A:Reference number: S37274

A:Accession: S37274

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1117 <MEV>

A:Cross-references: EMBL:X75156, NID:9404281, PDB:5404282

C:Superfamily: vaccinia virus 14k cell fusion protein

Query Match 90.3% Score 29; DB 2; Length 117;
Best Local Similarity 83.3% Pred. No. 6;
Matches 5: Conservative 1: Mismatches 0: Indels 0: Gaps 0:

QY 1 NDQVLF 6
11:111
Db 75 NDEVLF 80

RESULT 13
A04821

probable membrane protein p0633 - Escherichia coli

C:Species: Escherichia coli

GenCore version 4.5
Copyright (c) 1998 - 1999 GenProbes Ltd.

OM protein: protein search using sw model

Run on: 1999-06-22 11:01:19 Search time: 81.17 seconds
(without alignments)

3,980 Million cell updates/sec

Title: US-09-030-061-2

Percent score: 33

Sequence: 1 FERM1

Scoring table: BLOSUM62

Searched: 180763 seqs, 55169189 residues

Database:

SPIREMBL_8:
1: sp_fungi:
2: sp_human:
3: sp_invertebrate:
4: sp_mammal:
5: sp_mice:
6: sp_oranella:
7: sp_phage:
8: sp_plant:
9: sp_bacteria:
10: sp_protist:
11: sp_virus:
12: sp_vertebrate:
13: sp_unclassified:
14: sp_archaea:

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	33	100.0	333	11	098354	098354 myxoma virus
2	30	90.0	340	2	015194	015194 homo sapien
3	30	90.0	340	2	060226	060226 homo sapien
4	29	90.0	324	2	078536	078536 homo sapien
5	28	87.5	327	10	088714	088714 mus musc
6	30	90.0	348	14	027106	027106 methanobact
7	29	87.5	300	2	023079	023079 caenothabdi
8	29	87.5	345	1	011940	011940 caenothabdi
9	28	87.5	327	2	021023	021023 arabidopsis
10	28	87.5	345	2	024016	024016 lycopersicon
11	29	97.5	322	9	004305	004305 pseudomonas
12	29	87.5	340	9	053682	053682 staphylococ
13	29	87.5	322	11	027073	027073 human immun
14	29	87.5	322	11	056998	056998 human immun
15	29	87.5	322	11	057008	057008 human immun
16	29	87.5	322	11	054637	054637 halobacteri
17	29	87.5	322	11	054637	054637 halobacteri
18	29	87.5	322	11	054637	054637 halobacteri
19	29	87.5	322	11	054637	054637 halobacteri
20	29	87.5	322	11	054637	054637 halobacteri
21	29	87.5	322	11	054637	054637 halobacteri
22	29	87.5	322	11	054637	054637 halobacteri
23	29	87.5	322	11	054637	054637 halobacteri
24	29	87.5	322	11	054637	054637 halobacteri
25	29	87.5	322	11	054637	054637 halobacteri
26	29	87.5	322	11	054637	054637 halobacteri
27	29	87.5	322	11	054637	054637 halobacteri
28	29	87.5	322	11	054637	054637 halobacteri
29	29	87.5	322	11	054637	054637 halobacteri
30	29	87.5	322	11	054637	054637 halobacteri

ALIGNMENTS

RESULT	ID	PRELIMINARY	PRI	333 AA
098354	098354	PRELIMINARY	PRI	333 AA
AC	098354	PRELIMINARY	PRI	333 AA
DI	01-FEB-1997 (FERMBL_02) (CREATED)			
DI	01-FEB-1997 (FERMBL_02) (LAST SEQUENCE UPDATE)			
DI	01-NOV-1998 (FERMBL_08) (LAST ANNOTATION UPDATE)			
DE	POTATIVE SERPIN-LIKE PROTEIN			
OS	MYXOMA VIRUS			
OC	VIROSES; ESNA VIRUSES; NO RNA STAGE; POWDERHILL; HEPD; POWDERHILL			
OC	LEPORIPPOVIRUS			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-11			
EX	EXTRACTED: 95324099			
FA	FEIT F. REFERENCE S. CIFTI J. FASSY E. BOCHART-BARON C.			
KA	MILON A.			
BT	Myxomatosis is a myxoma virus-induced viral-like protein with			
PT	activity against intercalin-1 beta-converting enzyme.			
FL	1 VIRAL 70-800-800(1996)			
DR	EMBL: 060474; G1527065			
EV	PEAK: 060079; serpin01.1			
SO	SEQUENCE 333 AA; 36056 MW; BLOSUM62 CRC32;			
07	1 FERM1D 6			
DB	215 FERM1D 260			
Query Match	100.0%	Score 33	DB 11	Length 333
Best Local Similarity	100.0%	Prod. No. 0.01		
Motif	100.0%	Motif		
RESULT	2	PRELIMINARY	PRI	340 AA
ID	015194	PRELIMINARY	PRI	340 AA
AC	015194	PRELIMINARY	PRI	340 AA
DI	01-JAN-1998 (FERMBL_05) (CREATED)			
DI	01-JAN-1998 (FERMBL_05) (LAST SEQUENCE UPDATE)			
DI	01-NOV-1998 (FERMBL_08) (LAST ANNOTATION UPDATE)			
DE	HVAD2			
OS	HOMO SAPIENS (HUMAN)			
OC	HYPERALGIA; MYXOMA; ORFVIRUS; VITREOGEN; MAMMARY; EPIPLASMA; EPIPLASMA			
OC	CAHARFEN; HUMANIN; HOMO			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-11			
EX	EXTRACTED: 9223004			
FA	ISHIYAMA S. FAI M. JAMES M. JAMES M. JAMES M. JAMES M.			
KA	YAMANE Y. OGAWA M. NAKAMURA Y.			
BT	Sequence analysis of a 340-aa protein with a high degree of			
PT	that is homology with a high degree of homology with a high degree of			

CC METABOLISM
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-DELTA H:
 RX MEDLINE: 98037514
 RA SMITH D R, TROSCHEL-STANKI A, LEH H-M, JIROIS J,
 RA ALPERIN T, RASHIDZADEH P, BLAKLEY D, COOK P, GILBERT K,
 RA HARRISON D, HOANG I, KRAIG P, LUMM W, POTTER B, QIU D,
 RA SPADARONE R, VITAEF P, WANG Y, MIEZBOWSKI J, GIBSON R, JIWANI N,
 RA GARG A, BUSH T, SARTER P, DAVIELLO A, CHOPRA G M, BANISTER C J,
 RA SHERR G, GYAL A, PIERZWSKI S, CHOPRA G M, BANISTER C J,
 RA MAO T, GYAL A, PIERZWSKI S, CHOPRA G M, BANISTER C J,
 RT Complete genome sequence of *Methanobacterium thermoautotrophicum*
 RI delta functional analysis and comparative genomics
 RL J BACTERIOLOGY 179:7135-7155(1997)
 DR EMBL: AF000822 (3522227)
 SO SEQUENCE 348 AA: 34801 MW: 646466 GRC32

Query Match 90.9% Score 30: 28 14: Length 348:
 Best Local Similarity 83.3% Pred No: 32:
 Matches 5: Conservative 1: Mismatches 0: Indels 0: Gaps 0:

QY 1 FEDMTD 6
 DB 161 FEDMTD 166

RESULT 7
 ID 023078 PART: MINARY: PRT 108 AA
 AC 023078 (REMBL: 01, CREATED)
 DT 01-NOV-1996 (REMBL: 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1996 (REMBL: 06, LAST ANNOTATION UPDATE)
 DE (OSMT: 0031)
 GN 2037.6
 OS CAENORHABDITIS ELEGANS.
 CC EMBRYOTA: METAZOA: NEMATODA: SEPTENTRINA: PHAROTIA: PHAROTIDA:
 CC PHAROTIDA: PHAROTIDAE: PHAROTIDAE: PLEDERINAE: CAENORHABDITIS
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2:
 RX MEDLINE: 94150718
 RA WILSON R, AINSWORTH P, ANDERSON K, BAYNES C, BEERS M, BONFIELD J,
 RA PETERSON J, COOPER J, GILBERT K, GIBSON R, JIWANI N,
 RA DEAR S, DE Z, EHRIN F, FAVELLO A, FULTON L, GARNER A, GREEN P,
 RA HARKINS T, HILLER L, JETER M, JOHNSON L, JONES M, KESHAU J,
 RA KIRSTEN T, LAISTER N, LATRELL P, LIGHTNING J, LLOYD C,
 RA MURRAY A, MORTIMORE B, O'CALLAGHAN M, PARSONS J, PERCY C,
 RA PETERSON J, PETERSON J, SANDERS T, SHANKEN F, SMITH A,
 RA SONNHAMMER E, STADEN R, SUSTON J, THIERY-MEG J, THOMAS K,
 RA VAIDIN M, VARGAS K, WATSON P, WATSON A, WEINSTOCK L,
 RA WILKINSON-SPRAT J, WILKINSON P,
 RT 2.2 Mb of contiguous nucleotide sequence from chromosome III of *C. elegans*.
 RL NATURE 366:29-30(1994)
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2:
 RA GEISEL C, BRADSHAW H:
 RL SUBMITTED (01-1996) TO EMBL/GENBANK/EBI DATA BANKS
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2:
 RA WATSON R:
 RL SUBMITTED (01-1996) TO EMBL/GENBANK/EBI DATA BANKS
 DR EMBL: 064840: 31465791:
 SO SEQUENCE 308 AA: 34316 MW: 643004 GRC32

Query Match 87.3% Score 29: 28 3: Length 308:
 Best Local Similarity 83.3% Pred No: 47:

Matches 5: Conservative 1: Mismatches 0: Indels 0: Gaps 0:
 QY 1 FEDMTD 6
 DB 215 FEDMTD 220

RESULT 8
 ID 017980 PART: MINARY: PRT 346 AA
 AC 017980 (REMBL: 01, CREATED)
 DT 01-NOV-1996 (REMBL: 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1996 (REMBL: 06, LAST ANNOTATION UPDATE)
 DE C14C11.1 PROTEIN.
 GN C14C11.1
 OS CAENORHABDITIS ELEGANS.
 CC EMBRYOTA: METAZOA: NEMATODA: SEPTENTRINA: PHAROTIA: PHAROTIDA:
 CC PHAROTIDA: PHAROTIDAE: PHAROTIDAE: PLEDERINAE: CAENORHABDITIS
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2:
 RX MEDLINE: 94150718
 RA WILSON R, AINSWORTH P, ANDERSON K, BAYNES C, BEERS M, BONFIELD J,
 RA PETERSON J, COOPER J, GILBERT K, GIBSON R, JIWANI N,
 RA DEAR S, DE Z, EHRIN F, FAVELLO A, FULTON L, GARNER A, GREEN P,
 RA HARKINS T, HILLER L, JETER M, JOHNSON L, JONES M, KESHAU J,
 RA KIRSTEN T, LAISTER N, LATRELL P, LIGHTNING J, LLOYD C,
 RA MURRAY A, MORTIMORE B, O'CALLAGHAN M, PARSONS J, PERCY C,
 RA PETERSON J, PETERSON J, SANDERS T, SHANKEN F, SMITH A,
 RA SONNHAMMER E, STADEN R, SUSTON J, THIERY-MEG J, THOMAS K,
 RA VAIDIN M, VARGAS K, WATSON P, WATSON A, WEINSTOCK L,
 RA WILKINSON-SPRAT J, WILKINSON P,
 RT 2.2 Mb of contiguous nucleotide sequence from chromosome III of *C. elegans*.
 RL NATURE 366:32-38(1994)
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2:
 RA DO Z, GILLUNG S:
 RL SUBMITTED (01-1996) TO EMBL/GENBANK/EBI DATA BANKS
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2:
 RA WATSON R:
 RL SUBMITTED (01-1996) TO EMBL/GENBANK/EBI DATA BANKS
 DR EMBL: 064840: 31465791:
 SO SEQUENCE 346 AA: 34316 MW: 643004 GRC32

Query Match 87.3% Score 29: 28 3: Length 346:
 Best Local Similarity 83.3% Pred No: 53:
 Matches 5: Conservative 1: Mismatches 0: Indels 0: Gaps 0:

QY 1 FEDMTD 6
 DB 259 FEDMTD 258

RESULT 9
 ID 061923 PART: MINARY: PRT 327 AA
 AC 061923 (REMBL: 07, CREATED)
 DT 01-AUG-1996 (REMBL: 07, LAST SEQUENCE UPDATE)
 DT 01-AUG-1996 (REMBL: 06, LAST ANNOTATION UPDATE)
 DE C18G1.9 PROTEIN.
 GN C18G1.9
 OS CAENORHABDITIS ELEGANS.
 CC EMBRYOTA: METAZOA: NEMATODA: SEPTENTRINA: PHAROTIA: PHAROTIDA:
 CC PHAROTIDA: PHAROTIDAE: PHAROTIDAE: PLEDERINAE: CAENORHABDITIS
 RN (1)
 RP SEQUENCE FROM N.A.

024016
ID 024016 PRELIMINARY: PRT: 1240 AA.
AC 024016
DT 01-JAN-1996 (FREMELBEL 01, CREATED)
DT 01-JAN-1996 (FREMELBEL 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (FREMELBEL 01, LAST ANNOTATION UPDATE)
DE RESISTANCE COMPLEX PROTEIN 120/2.
OS 120/2.
OC HYPERSENSITIVITY SYNDROME (TOMATO).
OC TRACHEOPHYTES: EUPHYLLIPHYTES: SPERMATOPHYTES: MAGNOLIOPHYTES:
OC EUDICOTYLEDONS: ASTERIDAE: SOLANACEAE: SOLANACEAE: SOLANUM
RN 111
RP SEQUENCE FROM N.A.
RX MEDLINE: 97290204.
RA ORI N. J. ESHED Y. PARAN I. PRESTING G. AVIV D. TANKSLEY S.
RA ZAMIR D. FLUHR R.
RT The 120 family from the wild disease resistant locus 12 belongs to
RT the nucleotide binding, leucine-rich repeat superfamily of plant
RT resistance genes.
RI PLANT CELL 9:521-522(1997).
RU EMBL: AF094879: G2258317.
DR FEAM: P400560: LRR: 6.
DR PFAM: PF009311: NB-ARC: 1.
SC SEQUENCE 1240 AA, 14523 MW, 15539309 CIRC32.

Query Match 87.9% Score 29: DB 8: Length 1240
Best Local Similarity 83.3% Prod. No. 42e-02
Matches 5: Conservative 1: Mismatches 1: Indels 0: Gaps 0

QY 1 FEDMTD 6
DB 841 FEDMTD 846

024016
ID 024016 PRELIMINARY: PRT: 405 AA.
AC 024016
DT 01-NOV-1996 (FREMELBEL 01, CREATED)
DT 01-NOV-1996 (FREMELBEL 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (FREMELBEL 01, LAST ANNOTATION UPDATE)
DE HYPOHETICAL 42.2 Kd PROTEIN (ORF 3).
DS PSEUDOMONAS SP. (STRAIN K9740).
OS BACTERIA: PROTEOBACTERIA.
OC BACTERIA: PROTEOBACTERIA.
RN 111
RP SEQUENCE FROM N.A.
RX MEDLINE: 92339492.
RA ALIENSCHMIDT U. BOKRANZ M. FUCHS G.
RT Novel aerobic 2-aminobenzoate metabolism. Nucleotide sequence of the
RT plasmid carrying the gene for the flavoprotein 2-aminobenzoate-70A
RT monooxygenase/fluorase in a denitrifying pseudomonas sp.
RI EMBL: J04026: 297115-722(1992).
RU 1- SIMILARITY TO GENE 11 AND X PROTEINS (P154.9) FROM
OC BACTERIOPHAGE 12-2.
OC EMBL: M1154: 345973.
DR PIR: S24378: S24378.
KW HYPOTHETICAL PROTEIN: PLASMID.
SC SEQUENCE 372 AA, 42523 MW, 44336571 CIRC32.

Query Match 87.9% Score 29: DB 9: Length 472
Best Local Similarity 83.3% Prod. No. 58
Matches 5: Conservative 1: Mismatches 0: Indels 0: Gaps 0

QY 1 FEDMTD 6
DB 26 FEDMTD 31

RESULT 13

053682
ID 053682 PRELIMINARY PRI. 940 AA.
AC 053682:
DI 01-NOV-1996 (TREMRELEL. 01, CREATED)
DT 01-NOV-1996 (TREMRELEL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMRELEL. 06, LAST ANNOTATION UPDATE)
DE FR-RECTIN BINDING PROTEIN B.
DN ENB.
OS STAPHYLOCOCCUS AUREUS.
OC BACTERIA, FIRMICUTES, BACILLUS/CLUSTIDIUM GROUP: BACILLACEAE;
OC STAPHYLOCOCCUS.
RN 1)
RP SEQUENCE FROM N.A.
RC STRAIN-92204.
RX MEDLINE: 9211475.
RA TONSON R, STINAS C, WHITE H P, LINDEP M;
RI "Two different genes encode fibronectin binding proteins in
STAPHYLOCOCCUS AUREUS: the complete nucleotide sequence and
characterization of the second gene.";
FI FIB. 1, BIOCHEM. 202:1041-1049(1993).
DR EMBL: X60020, GENEID: 101170.
DP FRM. PROTEIN: 927-1033-37-11.
SQ SEQUENCE 340 AA; 10355 MW; DEAB050 CRO32.

Query Match 87.9% Score 29, FR 9, Length 340,
Best Local Similarity 83.3% Pred No. 16002.
Matches 5, Conservative 1, Mismatches 0, Indels 0, Gaps 0,
OY 1 FEDMT 6
DB 5 FEDMT 10

RESULT 14
077073 PRELIMINARY PRI. 92 AA.
AC 077073:
DI 01-NOV-1996 (TREMRELEL. 01, CREATED)
DT 01-NOV-1996 (TREMRELEL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMRELEL. 01, LAST ANNOTATION UPDATE)
DE ENVELOPE PROTEIN (FRAGMENT).
DN ENV.
OS HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1).
OC VIRUSES: RETROVIRUSES; RETROVIRIDAE; LENTIVIRUS.
RN 1)
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT MOTHER 566, 24-MONTH SAMPLE;
RA SIMONON A, KAMPINGA G.A., VAN DE PEPPE P, KAPITA E, MSELLATI P,
RA KOIKEN C, GOODSMITH J.;
FI STRMITFD (JUL-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: Z76325, E254051.
KW ENVELOPE PROTEIN.
FT NON-TER 1
FT NON-TER 92
SQ SEQUENCE 92 AA; 10170 MW; AD9E1E4 CRO32.

Query Match 87.9% Score 29, FR 11, Length 92,
Best Local Similarity 83.3% Pred No. 12.
Matches 5, Conservative 1, Mismatches 0, Indels 0, Gaps 0,
OY 1 FEDMT 6
DB 5 FEDMT 10

RESULT 15
076999 PRELIMINARY PRI. 92 AA.
AC 076999:
DI 01-NOV-1996 (TREMRELEL. 01, CREATED)
DT 01-NOV-1996 (TREMRELEL. 01, LAST SEQUENCE UPDATE)

DI 01-NOV-1996 (TREMRELEL. 06, LAST ANNOTATION UPDATE)
DE ENVELOPE PROTEIN (FRAGMENT).
DN ENV.
OS HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1).
OC VIRUSES: RETROVIRUSES; RETROVIRIDAE; LENTIVIRUS.
RN 1)
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT CHILD 566, 24-MONTH SAMPLE;
RA SIMONON A, KAMPINGA G.A., VAN DE PEPPE P, KAPITA E, MSELLATI P,
RA KOIKEN C, GOODSMITH J.;
FI STRMITFD (JUL-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: Z76323, E253624.
DR HEAM: PE00516, GP120/1.
KW ENVELOPE PROTEIN.
FT NON-TER 1
FT NON-TER 92
SQ SEQUENCE 92 AA; 10542 MW; FE4B240 CRO32.

Query Match 87.9% Score 29, DB 11, Length 92,
Best Local Similarity 83.3% Pred No. 12.
Matches 5, Conservative 1, Mismatches 0, Indels 0, Gaps 0,
OY 1 FEDMT 6
DB 5 FEDMT 10
Search completed, time = 1.99, 11:00:02
Job time: 167 sec



GenCore version 4.5
Copyright (c) 1993 - 1998 CompuGen Ltd

CM protein - protein search, using sw model

Run on: June 22, 1999, 10:56:39 ; Search time 61.72 seconds
(without alignment)

2.234 Million cell updates/sec

Title: US-09-030-061-3

Sequence: 1 EXTRACT

Scoring Table: BTCSUM62

Search for:

Database : A_Genesis_34 :

Pred ≥ 1 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	33	100.0	157	1	R92506	Interferon gamma
2	33	100.0	157	1	R93564	Human interleu-
3	33	100.0	157	1	R99568	Human mature inte-
4	33	100.0	157	1	R99569	Mouse mature inte-
5	33	100.0	157	1	R99569	Human interleu-
6	33	100.0	157	1	R44262	Murine protein (c-
7	33	100.0	157	1	R61276	Human interleu-
8	33	100.0	157	1	R61757	Interferon gamma
9	33	100.0	157	1	R62047	Interferon gamma
10	33	100.0	157	1	R615704	Interferon gamma
11	33	100.0	157	1	R62761	Mouse interleu-
12	33	100.0	157	1	R61972	Interferon gamma
13	33	100.0	157	1	R61479	Amplio acid (seap-
14	33	100.0	157	1	R62176	Interleukin-1
15	33	100.0	157	1	R62176	Interleukin-1
16	33	100.0	157	1	R62176	Interleukin-1
17	33	100.0	157	1	R62741	Interferon gamma
18	33	100.0	157	1	R62741	Interferon gamma
19	33	100.0	157	1	R62741	Interferon gamma
20	33	100.0	157	1	R62741	Interferon gamma
21	33	100.0	157	1	R62741	Interferon gamma
22	33	100.0	157	1	R62741	Interferon gamma
23	33	100.0	157	1	R62741	Interferon gamma
24	33	100.0	157	1	R62741	Interferon gamma
25	33	100.0	157	1	R62741	Interferon gamma
26	33	100.0	157	1	R62741	Interferon gamma
27	33	100.0	157	1	R62741	Interferon gamma
28	33	100.0	157	1	R62741	Interferon gamma
29	33	100.0	157	1	R62741	Interferon gamma
30	33	100.0	157	1	R62741	Interferon gamma
31	33	100.0	157	1	R62741	Interferon gamma
32	33	100.0	157	1	R62741	Interferon gamma
33	33	100.0	157	1	R62741	Interferon gamma
34	33	100.0	157	1	R62741	Interferon gamma
35	33	100.0	157	1	R62741	Interferon gamma
36	33	100.0	157	1	R62741	Interferon gamma
37	33	100.0	157	1	R62741	Interferon gamma
38	33	100.0	157	1	R62741	Interferon gamma
39	33	100.0	157	1	R62741	Interferon gamma
40	33	100.0	157	1	R62741	Interferon gamma
41	33	100.0	157	1	R62741	Interferon gamma
42	33	100.0	157	1	R62741	Interferon gamma
43	33	100.0	157	1	R62741	Interferon gamma

[illegible]

ALIGNMENTS

RESULT 1
R92506
ID R92506 standard, Protein: 157 AA.
AC R92506:
DT 02-SEP-1996 (first entry)
DE Interferon gamma producing leukocyte protein
KW interferon gamma, inducer, myxoma, immunocompetent cell, antiviral
KW antitumor, antisepsis, immunoregulatory, platelet-increasing agent,
KW therapy, fever, viral, cytotoxicity, granuloma, renal cancer, brain cancer,
KW granuloma, mycosis, endocarditis, dermatitis, allergy, viral infection, AIDS,
KW killer T-cell, interleukin-2, IL-2, tumor necrosis factor, TNF,
KW adoptive immunotherapy, monoclonal antibody.
OS Mus musculus. *mouse*, *murine*, *domesticated mouse*

FH Key Location/Qualifiers
 FI Misc. Difference To /Label Mct, Thr
 FI EP-692526-A2.
 PN 17-JAN-1996.
 PD 13-JUL-1995. 304906.
 PR 14-MAY-1994. JP-181182.
 PR 10-FEB-1995. JP-040572.
 PA (HAYH.) HAYASHIHARA SEIICHIRO KAKAKU
 PI KAKAKU S. FUKUSHIMA T. FUKUDA M. OHTSUKA H. OHTSUKA M.
 PI Tanimoto T. Ichiyose K.
 DR WPI: 95-070177/08.
 DR N-PSDB: T92506.
 FI Protein that induces gamma interferon prodn. in immunocompetent cells. Used with as activator of antitumor agent also induces cytotoxicity of killer cells.
 FI Chaim Z, Foa S, 10pp, English.
 CC This sequence represents the interferon gamma (IFNgamma) inducer protein of the livestock. This protein induces IFNgamma production in immunocompetent cells. The protein is useful as an antiviral, antitumor, antileish, immunoregulatory and pleiotropic inducing agent. It can be used for treating or preventing AIDS, hairy-cell leukemia, myeloid leukemia, aplasia, myeloid leukemia, rheumatism and arthritis. This protein can also be used to induce IFNgamma production in cultured cells. The IFNgamma inducer strongly induces cytotoxicity of killer T cells and when used with interleukin-2 (IL-2) and tumor necrosis factor (TNF) may improve the effect of reduce side effects) of adopting immunotherapy in tumors. The DNA coding this sequence can be used to produce the protein which can then be purified for use with using monoclonal antibodies.
 CC Sequence 157 AA:

Supply Method	DB 1:	Length 15:
100.00	Scale 33:	
100.00	Prod. No. 33:	

1 EXLINK 7
1 1 1 1
122 EV+EV 138

RESULT	2
R99564	
ID	R99564 standard; Protein; 157 AA

[illegible]

Query Match 100.0% Score 33: DB 1: Length 157
 Best Local Similarity 100.0% Pred. No. 2.3:
 Mismatches 0: Indels 0: Gaps 0

1 FKLLKK 7
 134 FKLLKK 140

RESULT 4
 ID R99559 Standard: Protein: 157 AA.
 AC R99559: (first entry)
 DT 29-SEP-1996
 PF Mouse mature interferon-gamma inducer protein.
 KW Interferon-gamma inducer protein; IFN-gamma; antiviral; virocid;
 KM antitumor; antibacterial; immunoregulator; adoptive immunotherapy;
 OS Mus sp.
 FH Key
 FT misc.difference 70
 FI Location/Qualifiers
 FT misc.difference 70 /label= 11e, Thr
 FN DE-212931-A2.
 PD 22-MAY-1996.
 PR 10-NOV-1995: J08055.
 PR 15-NOV-1995: JP-304203.
 PR 23-FEB-1995: JP-058240.
 PR 10-MAR-1995: JP-078357.
 PR 18-SEP-1995: JP-262052.
 PR 29-SEP-1995: JP-274988.
 PA (HAYASHI) HAYASHIBARA SEIBUTSU KAGAKU.
 PI Fukuda S, Kohno K, Kunikida T, Kurimoto M, Okamura H;
 PI Taniguchi M, Tanimoto T, Torioka K, Ushio S;
 PI WEI: 96-25297/26.
 DR N-PSDB: T32403.
 FT CNA encoding interferon gamma prodn. inducing polypeptide - useful
 PT to treat and prevent, e.g. viral disease, malignancies and immune
 PT disorders
 PS Example A-3-2: Page 36-37: 48pp: English.
 CC A novel mouse protein (R99559) induces interferon gamma (IFN-gamma)
 CC prodn. by immunocompetent cells. Its sequence was deduced from
 CC that of a cDNA clone (T32403) isolated from a mouse liver library.
 CC Recombinant IFN-gamma inducer protein can be produced in high yields
 CC using host cells, esp. Escherichia coli, transformed with a vector
 CC carrying the cDNA.
 CC Sequence 157 AA.
 SO Sequence 157 AA.

Query Match 100.0% Score 33: DB 1: Length 157
 Best Local Similarity 100.0% Pred. No. 2.3:
 Mismatches 0: Indels 0: Gaps 0

1 FKLLKK 7
 134 FKLLKK 140

RESULT 5
 ID R99560 Standard: Protein: 193 AA.
 AC R99560: (first entry)
 DT 29-SEP-1996
 PF Mouse mature interferon-gamma inducer protein.
 KW Interferon-gamma inducer protein; IFN-gamma; antiviral; virocid;
 KM antitumor; antibacterial; immunoregulator; adoptive immunotherapy;
 OS Mus sp.
 FH Key
 FT misc.difference 70
 FI Location/Qualifiers
 FT misc.difference 70 /label= 11e, Thr
 FN DE-212931-A2.
 PD 22-MAY-1996.
 PR 10-NOV-1995: J08055.
 PR 15-NOV-1995: JP-304203.
 PR 23-FEB-1995: JP-058240.
 PR 10-MAR-1995: JP-078357.
 PR 18-SEP-1995: JP-262052.
 PR 29-SEP-1995: JP-274988.
 PA (HAYASHI) HAYASHIBARA SEIBUTSU KAGAKU.
 PI Fukuda S, Kohno K, Kunikida T, Kurimoto M, Okamura H;
 PI Taniguchi M, Tanimoto T, Torioka K, Ushio S;
 PI WEI: 96-25297/26.
 DR N-PSDB: T32403.
 FT CNA encoding interferon gamma prodn. inducing polypeptide - useful
 PT to treat and prevent, e.g. viral disease, malignancies and immune
 PT disorders
 PS Example A-3-2: Page 36-37: 48pp: English.
 CC A novel mouse protein (R99560) induces interferon gamma (IFN-gamma)
 CC prodn. by immunocompetent cells. Its sequence was deduced from
 CC that of a cDNA clone (T32403) isolated from a mouse liver library.
 CC Recombinant IFN-gamma inducer protein can be produced in high yields
 CC using host cells, esp. Escherichia coli, transformed with a vector
 CC carrying the cDNA.
 CC Sequence 193 AA.
 SO Sequence 193 AA.

DE Human interferon-gamma inducer protein.
 KW Interferon gamma inducer protein, IFN-gamma; antiviral; virology;
 KW anti-tumour; antihypertensive; immunoregulator; adoptive immunotherapy;
 KW +therapy; cancer.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT peptide 1..36
 FT /label= Leader-peptide
 FT protein 37..193
 FT /label= Mat-protein
 FT misc-difference 109
 FT /label= Ile, Thr
 PN EP-71293; A2.
 PD 22-MAY-1995.
 PE 10-NOV-1995; 308055.
 PR 15-NOV-1994; JP-304203.
 PR 23-FEB-1995; JP-058240.
 PR 10-MAR-1995; JP-078357.
 PR 18-SEP-1995; JP-242062.
 PR 29-SEP-1995; JP-274988.
 PA (HAYR.) HAYASHIBARA SEIJIYUJI KAGAKU.
 PI Fukuoka S. Kunita T. Kunita M. Okamura H.
 PI Tadavichi M. Tadavichi T. Tadavichi K. Ushio S.
 DR N-PSDB: T2414.
 DE DNA encoding for interferon-gamma inducer-inducing polypeptide - useful
 PT to treat and prevent, e.g. viral disease, malignancies and immune
 PT disorders.
 PS Claim 6, Page 41-42, 48pp. English.
 CC The mature portion of a novel human protein (P24550) induces
 CC interferon-gamma (IFN-gamma) production by immunocompetent cells. It
 CC is the product of a cDNA clone (T2404) cDNA from a human liver
 CC library. The protein enhances the cytotoxicity of killer cells
 CC and/or induces the formation of killer cells (e.g. NK cells,
 CC lymphocyte-activating killer (LAK) cells, and cytotoxic T-cells).
 CC The mature protein (see also R99558) is useful as an antiviral,
 CC antitumor, antibacterial, immunoregulatory and blood platelet-
 CC enhancing agent and can be used in adoptive immunotherapy. It is
 CC also used to raise monoclonal antibodies.
 SO Sequence 193 AA.
 Query Match 100.0%; Score 33; DB 1; Length 193;
 Best Local Similarity 100.0%; Prod. No. 2.3;
 Mismatch 0; Mismatches 0; Indels 0; Gaps 0;
 DB 170 FKILKK 175
 OR 1 FKILKK 7
 ID W24258 standard; Protein: 157 AA.
 AC W24258.
 DT 15-OCT-1997 (first entry)
 DE Mature protein for induction of interferon-gamma.
 KW Interferon gamma immunocompetent cell; malignant tumour;
 KW viral disease; bacterial infection; immune disease.
 OS Mus musculus.
 FH Key Location/Qualifiers
 FT misc-difference 70
 FT /note= "Encoded by AYI"
 PN J09157180-A.
 PD 17-JUN-1997.
 PE 24-JAN-1995; 028722.
 PR 04-OCT-1995; JP-279906.
 PR 10-MAR-1995; JP-078357.
 PR 29-SEP-1995; JP-274988.
 PA (HAYR.) HAYASHIBARA SEIJIYUJI KAGAKU.
 PI WPI: 97-369361/34.
 DR N-PSDB: T80209.
 PT A drug containing a polypeptide which induces interferon-gamma -

PT useful for treating e.g. malignant tumours, viral, bacterial or
 PT immune diseases.
 PS Disclosure, Page 10-11, 13pp. Japanese.
 CC This sequence represents a protein which induces interferon-gamma
 CC production in immunocompetent cells. This protein may be used as
 CC the major component in a drug for the prevention and treatment of
 CC e.g. malignant tumours, viral diseases, bacterial infections and
 CC immune diseases.
 SO Sequence 157 AA.
 Query Match 100.0%; Score 33; DB 1; Length 157;
 Best Local Similarity 100.0%; Prod. No. 2.3;
 Mismatch 0; Mismatches 0; Indels 0; Gaps 0;
 DB 134 FKILKK 140
 OR 1 FKILKK 7
 ID W31757 standard; Protein: 193 AA.
 AC W31757.
 DT 15-JAN-1998 (first entry)
 DE Interferon gamma inducing factor 2 (IGIF-2) R1401 variant.
 KW Interferon gamma inducing factor 2, IGIF-2; leucocyte; lymphocyte; human;
 KW interleukin; interferon; interferon-inducer; interferon; interleukin;
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT misc-difference 140
 PN W31757
 ID W31757 standard; Protein: 193 AA.
 AC W31757.
 DT 15-JAN-1998 (first entry)
 DE Interferon gamma inducing factor 2 (IGIF-2) R1401 variant.
 KW Interferon gamma inducing factor 2, IGIF-2; leucocyte; lymphocyte; human;
 KW interleukin; interferon; interferon-inducer; interferon; interleukin;
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT misc-difference 140

11 Label: IL12P
 12 Accession: W22047
 13 Accession: W22047
 14 Accession: W22047
 15 Accession: W22047
 16 Accession: W22047
 17 Accession: W22047
 18 Accession: W22047
 19 Accession: W22047
 20 Accession: W22047
 21 Accession: W22047
 22 Accession: W22047
 23 Accession: W22047
 24 Accession: W22047
 25 Accession: W22047
 26 Accession: W22047
 27 Accession: W22047
 28 Accession: W22047
 29 Accession: W22047
 30 Accession: W22047
 31 Accession: W22047
 32 Accession: W22047
 33 Accession: W22047
 34 Accession: W22047
 35 Accession: W22047
 36 Accession: W22047
 37 Accession: W22047
 38 Accession: W22047
 39 Accession: W22047
 40 Accession: W22047
 41 Accession: W22047
 42 Accession: W22047
 43 Accession: W22047
 44 Accession: W22047
 45 Accession: W22047
 46 Accession: W22047
 47 Accession: W22047
 48 Accession: W22047
 49 Accession: W22047
 50 Accession: W22047
 51 Accession: W22047
 52 Accession: W22047
 53 Accession: W22047
 54 Accession: W22047
 55 Accession: W22047
 56 Accession: W22047
 57 Accession: W22047
 58 Accession: W22047
 59 Accession: W22047
 60 Accession: W22047
 61 Accession: W22047
 62 Accession: W22047
 63 Accession: W22047
 64 Accession: W22047
 65 Accession: W22047
 66 Accession: W22047
 67 Accession: W22047
 68 Accession: W22047
 69 Accession: W22047
 70 Accession: W22047
 71 Accession: W22047
 72 Accession: W22047
 73 Accession: W22047
 74 Accession: W22047
 75 Accession: W22047
 76 Accession: W22047
 77 Accession: W22047
 78 Accession: W22047
 79 Accession: W22047
 80 Accession: W22047
 81 Accession: W22047
 82 Accession: W22047
 83 Accession: W22047
 84 Accession: W22047
 85 Accession: W22047
 86 Accession: W22047
 87 Accession: W22047
 88 Accession: W22047
 89 Accession: W22047
 90 Accession: W22047
 91 Accession: W22047
 92 Accession: W22047
 93 Accession: W22047
 94 Accession: W22047
 95 Accession: W22047
 96 Accession: W22047
 97 Accession: W22047
 98 Accession: W22047
 99 Accession: W22047
 100 Accession: W22047

CC of treat (IGF-2) induction of proliferation, differentiation or maturation
 CC of leucocytes or lymphocytes, especially in relation to tissue damage
 CC associated with inflammation.
 SO Sequence 193 AA:
 Query Match 100.0% Score 33 DB 1 Length 193
 Best Local Similarity 100.0% Pred. No. 2.8:
 Matches 7: Conservative 0: Mismatches 0: Indels 0: Gaps 0
 0Y 1 FKLLKK 7
 1111111
 Db 170 FKLLKK 176
 RESULT 10
 W15704
 ID W15704 standard: peptide: 157 AA.
 DT 26-JAN-1998 (first entry)
 AC W15704:
 DE Mouse interferon-gamma inducer protein.
 KW Interferon-gamma, IFN-gamma; antiviral; antineoplastic; radiotherapy;
 KW immunoregulatory; antitumor agent; chemotherapy; leukopenia;
 KW lymphocyte-growth; immunoregulatory; killer cell;
 KW chemokine; interleukin; killer cell;
 OS Mus musculus.
 FT Misc-difference 70
 FT 100.0% /Label= Mol, Thr
 FN EP 767178-A1.
 PU 09-APR-1997.
 PF 26-SEP-1996: 306997.
 PR 20-SEP-1996: JP-269105.
 PR 26-SEP-1995: JP-270725.
 PR 25-FEB-1996: JP-067434.
 PA (HAYR) HAYASHIMURA SEIBUTSU KAGAKU
 PI Akita K, Fujii M, Kurimoto M, Nakada Y, Tanimoto H
 DR WPI: 97-265381/19.
 DR N-PSDB: T60536.
 PT Human protein that induces interferon-gamma protein, in
 PT tumours and as antimicrobial agent etc.
 PS Disclousure: Page 23: 26pp, English.
 CC This present sequence represents a novel protein from mouse liver cells,
 CC which induces interferon-gamma (IFN-gamma) production in immunocompetent
 CC cells. This protein enhances cytotoxicity of killer cells and induces
 CC their formation. It is used as an antineoplastic agent for antitumor
 CC immunotherapy or antiviral (including anti-AIDS) or antibacterial agent,
 CC and in the treatment of atopic or immune system disease, e.g. asthma,
 CC hay fever or leukaemia. When formulated with interleukin-3, it is also
 CC used to treat leukopenia and thrombocytopenia associated with
 CC radiotherapy or chemotherapy of leukaemia and other cancers. When used
 CC in antitumor immunotherapy, this novel protein significantly improves
 CC the immunotherapeutic effect of interferon-2 (IFN-2), compared with use
 CC of IFN-2 alone, either when administered to the patient (before
 CC administration of IFN-2) or by addition to the medium in which cells
 CC (intended for return to the patient) are being grown.
 SO Sequence 157 AA:
 Query Match 100.0% Score 33 DB 1 Length 157
 Best Local Similarity 100.0% Pred. No. 2.3:
 Matches 7: Conservative 0: Mismatches 0: Indels 0: Gaps 0
 0Y 1 FKLLKK 7
 1111111
 Db 132 FKLLKK 138
 RESULT 11
 W15701
 ID W15701 standard: protein: 157 AA.
 AC W15701:

DT 26-JAN-1998 (first entry)
 DE Interferon gamma (human protein)
 KW Interferon gamma, IFN-gamma, antiviral, antineoplastic, radiotherapy,
 KW immunoregulatory, antitumor agent, chemotherapy, leukaemia,
 KW "Thymus" (first), immunoregulatory, cell surface, haemostasis,
 KW rheumatism, interleukin, killer cell
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Misc-difference 73
 FT Ep-76/178-A1, /label= Ile, Thr
 PN 05-APR-1997
 PD 26-SEP-1996: 306997.
 PR 20-SEP-1996: IP-269105
 PR 25-SEP-1996: IP-269105
 PR 24-FEB-1996: IP-067434
 PA (HAYB) HAYASHIBARA SEIICHIRO KAKAKU
 PI AKIYAMA T, TAJIMA M, KIMURA Y, TAJIMA T,
 DF WPI: 97-205841/15
 PT Human protein, this protein interferon-gamma protein in
 FT Immunocompetent cells, useful for adoptive immuno therapy of
 FT tumors and as antimicrobial agent etc.
 PS Claim 8: Page 209 26pp. English.
 CC The present sequence represents a novel protein from human cells, which
 CC induces interferon-gamma (IFN gamma) production in immunocompetent cells
 CC This protein enhances cytotoxicity of killer cells and induces their
 CC formation. It is used as an antitumor agent for antitumor
 CC immunotherapy. An antiviral (including anti-AIDS) or antineoplastic agent,
 CC and in the treatment of allergic or immune system diseases, e.g., asthma,
 CC hay fever or rheumatism. When formulated with interleukin-3, it is also
 CC used to treat leukaemia and lymphoproliferative disorders associated with
 CC radiotherapy or chemotherapy of leukaemia and other cancers. When used in
 CC antitumor immunotherapy, this novel protein significantly improves the
 CC immunotherapeutic effect of interleukin-3 (IL-3). Compared with use of
 CC IL-3 alone, either when administered to the patient (before
 CC administration of IL-3) or by addition to the medium in which cells
 CC (intended for return to the patient) are being grown.
 SQ Sequence 157 AA:

Query Match 100.0%: Score 33; DB 1; Length 157;
 Best Local Similarity: 100.0%: Prod NO. 27;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 FKILIKK 7
 Db 134 FKILIKK 140
 RESULT 12
 W45592
 ID W45592 standard, Protein, 133 AA.
 AC W45592;
 DT 21-MAY-1998 (first entry)
 DE Antigen 333 antigen of human interferon-gamma.
 KW Interferon gamma, IFN-gamma, mouse, cytokine, 16IF, interferon-gamma,
 KW Interferon gamma, IFN-gamma, mouse, cytokine, 16IF, interferon-gamma,
 KW Interferon gamma, IFN-gamma, mouse, cytokine, 16IF, interferon-gamma,
 KW Interferon gamma, IFN-gamma, mouse, cytokine, 16IF, interferon-gamma,
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 41..47 "beta-1 region"
 FT Region 51..59 "beta-2 region"
 FT Region 64..66 "beta-3 region"
 FT Region 83..88 "beta-4 region"
 FT Region 93..102 "beta-5 region"
 FT Region 108..113 "beta-6 region"
 FT Region 115..120 "beta-6 region"

FT FT /note= "beta-2 region"
 FT Region 137..143 /note= "beta-8 region"
 FT Region 147..153 /note= "beta-9 region"
 FT Region 160..164 /note= "beta-10 region"
 FT Region 170..175 /note= "beta-11 region"
 FT Region 187..191 /note= "beta-12 region"
 FT FT
 PN W09744468-A1.
 PD 27-NOV-1997.
 PR 16-MAY-1997: D07982.
 PR 16-MAY-1997: US-055143.
 PA (SCHE) SCHEPPING CORP.
 PI BAZAN TF, HARDMAN GT, KASTELAIN PA, SANA TF, TIMANS JO,
 DF WPI: 98-018025/22.
 DR N-PSDB: W05368.
 PT Antagonist of human interleukin-1 gamma, used for treating
 FT Immunological disorders caused by human IL-1-gamma
 PS Disclosure: Pages 34-55, 61pp. English.
 CC The present sequence represents human interleukin-1 gamma (IL-1 gamma).
 CC The protein is the human equivalent of a mouse cytokine, 16IF, which
 CC induces certain T cells to produce interferon gamma. Human IL-1 gamma
 CC and mouse 16IF show 71% identity at the nucleotide level and
 CC approximately 65% identity at the amino acid level. Antagonists of
 CC IL-1 gamma, e.g., antibodies, can be used in a method for treating a
 CC condition caused by human IL-1 gamma. The antibodies can also be used
 CC in diagnostic assays. The IL-1 gamma protein can be covalently
 CC conjugated to polychloroethyl glycol or to a polypeptide, and the fusion
 CC protein used in a pharmaceutical composition for supplying the
 CC biological activity of IL-1 gamma. Conditions that can be treated using
 CC the human IL-1 gamma protein include immunological disorders, allergies,
 CC and infectious diseases. The IL-1 gamma can also be used to detect the
 CC presence of the protein or its receptor.
 SQ Sequence 193 AA:

Query Match 100.0%: Score 33; DB 1; Length 193;
 Best Local Similarity: 100.0%: Prod NO. 28;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 FKILIKK 7
 Db 170 FKILIKK 176
 RESULT 13
 W47429
 ID W47429 standard, Protein, 133 AA.
 AC W47429;
 DT 05-JUN-1998 (first entry)
 DE Interferon-gamma production inducer
 KW Interferon gamma, IFN-gamma, production inducer, gene therapy,
 KW immunocompetent cell, cytotoxic, antitumor, antineoplastic,
 KW Viral infection, bacterial infection, immune disease.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..36 /label= sig-peptide
 FT P-193 /label= 193
 FT Misc-difference 109 /label= mat-peptide
 FT Region 109 /label= Ile, Thr
 PN 07-APR-1998.
 PD 27-JUN-1997: 304616.
 PR 27-JUN-1997: JP-185305.
 PA (HAYB) HAYASHIBARA SEIICHIRO KAKAKU,
 PI KURIMOTO M, OKURA T, TORIJOE K,
 DF WPI: 98-04414/05.
 DR N-PSDB: V15825, V15826.

Genome version 4.5
 Copyright 1998-1999 Washington U.S.

OM protein - protein search using sw model

Run on: June 22, 1999, 10:58:45 ; Search time 61.51 Seconds

(Without alignments)
 4.263 Million cell updates/sec

Title: US-09-030-061-3

Perfect score: 33

Sequence: 1 FKILKK 7

S.W.I.T. Value: PIR-SW62

Searched: 11678 seqs 7746341 residues

Database: PIR-SW62

1: PIR-SW62
 2: PIR-SW62
 3: PIR-SW62
 4: PIR-SW62

Pred. No. 7: The number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	192	S60226	Cytokine IGIF - mouse
2	32	97.0	214	TC4747	cytochrome c
3	31	93.9	429	S62793	Chromosomal replic
4	30	90.9	144	IVPBD	small T antigen -
5	29	87.9	379	S55845	3-isopropylmalate
6	29	87.9	1024	RN208F	DNA-directed RNA p
7	26	87.9	403	H65970	hypothetical prote
8	26	84.9	316	1 TWB2P	transcriptin In1
9	26	84.9	328	S51594	peroxidase (EC 1.1
10	26	84.8	255	143157	peptide synthetase
11	26	84.8	216	S26299	transcription init
12	26	84.8	216	S26299	transcription init
13	26	84.8	32	H70153	hypothetical prote
14	26	84.8	101	S71747	hypothetical prote
15	26	84.8	811	S57149	probable membrane
16	26	84.8	487	A40711	RNA polymerase II
17	26	84.8	431	E71050	hypothetical prote
18	26	81.9	211	HMPHA	hyaluronidase
19	26	81.9	146	1466	dydin beta heavy
20	26	81.9	146	1466	dydin beta heavy
21	26	81.9	146	1466	dydin beta heavy
22	26	81.9	146	1466	dydin beta heavy
23	26	81.9	146	1466	dydin beta heavy
24	26	81.9	146	1466	dydin beta heavy
25	26	81.9	146	1466	dydin beta heavy
26	26	81.9	146	1466	dydin beta heavy
27	26	81.9	146	1466	dydin beta heavy
28	26	81.9	146	1466	dydin beta heavy
29	26	81.9	146	1466	dydin beta heavy
30	26	81.9	146	1466	dydin beta heavy
31	26	81.9	146	1466	dydin beta heavy
32	26	81.9	146	1466	dydin beta heavy
33	26	81.9	146	1466	dydin beta heavy
34	26	81.9	146	1466	dydin beta heavy
35	26	81.9	146	1466	dydin beta heavy
36	26	81.9	146	1466	dydin beta heavy
37	26	81.9	146	1466	dydin beta heavy
38	26	81.9	146	1466	dydin beta heavy
39	26	81.9	146	1466	dydin beta heavy
40	26	81.9	146	1466	dydin beta heavy

40	27	81.8	409	2	201396	3-isopropylmalate
41	27	81.8	227	2	S60226	cytochrome c
42	27	81.8	157	2	S60226	cytochrome c
43	27	81.8	157	2	A70381	hypothetical prote
44	27	81.8	412	2	S71994	hypothetical prote
45	26	78.8	445	2	B69744	phosphatase

ALIGNMENTS

RESULT 1

S60226

Cytokine IGIF - mouse

CSpecies: Mus musculus (house mouse)

Accession: S60226

Accession: S60226

Accession: S60226

Accession: S60226

Accession: S60226

Accession: S60226

Accession: S60226

Accession: S60226

Accession: S60226

Accession: S60226

Accession: S60226

Accession: S60226

Accession: S60226

Accession: S60226

Accession: S60226

Accession: S60226

Accession: S60226

Accession: S60226

Accession: S60226

Accession: S60226

Accession: S60226

Accession: S60226

Accession: S60226

Accession: S60226

Accession: S60226

Accession: S60226

Accession: S60226

Accession: S60226

Accession: S60226

Accession: S60226

Accession: S60226

RESULT 14

S74767

Hypothetical protein slr1066 - *Synechocystis* sp. (strain PCC 6803)C:Species: *Synechocystis* sp.

A:Variety: PCC 6803

C:Date: 25-Apr-1997 #update_revision: 25-Apr-1997 #text_change: 21-Aug-1998

C:Accession: S74767

R:Kobayashi, T.; Saito, S.; Kohani, H.; Tanaka, A.; Asanuma, E.; Nakamura, Y.; Miyajima, N.; Ohta, Y.; Chikama, S.; Shigeno, S.; Inouchi, C.; Wada, Y.; Watanabe, A.; Yamada, M.; Yasuda

DNA Res. 3, 109-116, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp.

A:Reference: Nature, 379, 690-693, 1996

A:Accession: S74767

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1401 <K&N>

A:Cross-reference: EMBL:U99001, GI:AA001339, NID:0161897, FID:0107051, PID:01651992

A:Note: the nucleotide sequence was submitted to the EMBL data library, June 1996

Query Match

84.8% Score 28; DB 2; Length 401;

Best local similarity 71.4%; Pred. No. 35;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERLIKK 7

1111111

DB 139 ERLIKK 145

RESULT 15

S57149

Probable, tentative, putative, YH1125, yeast (*Saccharomyces cerevisiae*)

N:Alternate names: hypothetical protein J7050

C:Species: *Saccharomyces cerevisiae*

C:Date: 23-Aug-1995 #update_revision: 06-Sep-1995 #text_change: 14-Nov-1997

C:Accession: S57149

R:Rosen, M.; Koevler, P.; Euliam, R.D.

submitted to the Protein Sequence Database, September 1995

A:Reference number: S56848

A:Accession: S57149

A:Molecule type: DNA

A:Residues: 1441 <R&S>

A:Cross-reference: EMBL:U99001, NID:0161897, FID:0107051, PID:01651992

C:Genetics:

A:Map position: 108

C:Keywords: transmembrane protein

Query Match

84.8% Score 28; DB 2; Length 811;

Best local similarity 71.4%; Pred. No. 71;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERLIKK 7

1111111

DB 255 YERLIKX 261

Search completed: June 22, 1999, 10:58:47
Job time: 14 sec



IN: (N) N-1998 (TREM) 01 AND: (N) N-1998 (TREM) 02.
 SIMILARITY: 71.4% Pred. No. 99;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0.

1 PK LINK 7
 ID 506 PKLINK 512

RESULT 4
 ID 086122 PRELIMINARY PRT 258 AA.
 AC 086122;
 DT 01-NOV-1998 (TREM) 08, CREATED)
 DT 01-NOV-1998 (TREM) 08, LAST SEQUENCE UPDATE)
 DE 01-NOV-1998 (TREM) 08, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL 30.1 K0 PROTEIN.
 OS BOPFELIA BOPFELI (TIME DISEASE EPIDEMIOLOGY).
 OC BACTERIA: SPIROCHAETALES: SPIROCHAETACEAE: BORRELIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-297;
 RX MEDLINE: 96342380.
 RA AKINS D.R.; BOPFELIA S.F.; BOPFELIA T.S.; SHEVCHENKO, V.; WARR S.T.;
 RA LI M.; NORRARD M.V.; RADOLF J.D.;
 RT "Evidence for in vivo but not in vitro expression of a Borrelia
 burgdorferi outer surface protein P (OspP) homologous to
 P1 MOL. MICROBIOL. 18:507-520(1995).
 RL [2]
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-297;
 RA AKINS D.R.;
 RE SUBMITTED (JUN-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]
 RP SEQUENCE FROM N.A.
 PC STRAIN-297;
 RA AKINS D.R.;
 RE SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: U30617; G3109517;
 KW HYPOTHETICAL PROTEIN.
 SV SEQUENCE 194 AA. 22913 MW. 19290270 CIRC32.

Query Match 87.94; Score 29; DB 9; Length 258;
 Best Local Similarity 71.4%; Pred. No. 47;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0.

1 PKLINK 7
 ID 194 PKLINK 192

RESULT 5
 ID 088749 PRELIMINARY PRT 194 AA.
 AC 088749;
 DT 01-NOV-1998 (TREM) 08, CREATED)
 DT 01-NOV-1998 (TREM) 08, LAST SEQUENCE UPDATE)
 DE 01-NOV-1998 (TREM) 08, LAST ANNOTATION UPDATE)
 DE INTERLEUKIN-18.
 GN IL-18.
 OS RATTUS NORVEGICUS (RAT).
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:
 OC EUMETAZOA: CORDONATA: MOLLUSCA: MOLLUSCA: LITTORALIA: LITTORALIA:
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE DAWLEY: TISSUE-WHOLE BRAIN;
 RA CULHANE A.C.; HALL M.D.; ROTHWELL N.J.; LUTHERSHI G.N.;
 RT "IL-18 is a novel member of the IL-1 family of cytokines.
 BL MOL. PSYCH. 3:362-366(1998).
 DR EMBL: AJ222813; F1315191;
 FT CHAIN 194
 SC SEQUENCE 194 AA. 22913 MW. 19290270 CIRC32.

IN: (N) N-1998 (TREM) 01 AND: (N) N-1998 (TREM) 02.
 SIMILARITY: 71.4% Pred. No. 99;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0.

1 PK LINK 7
 ID 506 PKLINK 512

RESULT 4
 ID 086122 PRELIMINARY PRT 258 AA.
 AC 086122;
 DT 01-NOV-1998 (TREM) 08, CREATED)
 DT 01-NOV-1998 (TREM) 08, LAST SEQUENCE UPDATE)
 DE 01-NOV-1998 (TREM) 08, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL 30.1 K0 PROTEIN.
 OS BOPFELIA BOPFELI (TIME DISEASE EPIDEMIOLOGY).
 OC BACTERIA: SPIROCHAETALES: SPIROCHAETACEAE: BORRELIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-297;
 RX MEDLINE: 96342380.
 RA AKINS D.R.; BOPFELIA S.F.; BOPFELIA T.S.; SHEVCHENKO, V.; WARR S.T.;
 RA LI M.; NORRARD M.V.; RADOLF J.D.;
 RT "Evidence for in vivo but not in vitro expression of a Borrelia
 burgdorferi outer surface protein P (OspP) homologous to
 P1 MOL. MICROBIOL. 18:507-520(1995).
 RL [2]
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-297;
 RA AKINS D.R.;
 RE SUBMITTED (JUN-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]
 RP SEQUENCE FROM N.A.
 PC STRAIN-297;
 RA AKINS D.R.;
 RE SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: U30617; G3109517;
 KW HYPOTHETICAL PROTEIN.
 SV SEQUENCE 194 AA. 22913 MW. 19290270 CIRC32.

Query Match 87.94; Score 29; DB 9; Length 258;
 Best Local Similarity 71.4%; Pred. No. 47;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0.

1 PKLINK 7
 ID 194 PKLINK 192

RESULT 5
 ID 088749 PRELIMINARY PRT 194 AA.
 AC 088749;
 DT 01-NOV-1998 (TREM) 08, CREATED)
 DT 01-NOV-1998 (TREM) 08, LAST SEQUENCE UPDATE)
 DE 01-NOV-1998 (TREM) 08, LAST ANNOTATION UPDATE)
 DE INTERLEUKIN-18.
 GN IL-18.
 OS RATTUS NORVEGICUS (RAT).
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:
 OC EUMETAZOA: CORDONATA: MOLLUSCA: MOLLUSCA: LITTORALIA: LITTORALIA:
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE DAWLEY: TISSUE-WHOLE BRAIN;
 RA CULHANE A.C.; HALL M.D.; ROTHWELL N.J.; LUTHERSHI G.N.;
 RT "IL-18 is a novel member of the IL-1 family of cytokines.
 BL MOL. PSYCH. 3:362-366(1998).
 DR EMBL: AJ222813; F1315191;
 FT CHAIN 194
 SC SEQUENCE 194 AA. 22913 MW. 19290270 CIRC32.

FT CHAIN 22 228 PEPTIDASE 1
 FT ACT SITE 60 60 BY SIMILARITY
 FT ACT SITE 64 64 DISTAL HISTIDINE (BY SIMILARITY)
 FT ACT SITE 192 192 PROXIMAL HISTIDINE (HEME AXIAL LIGAND)
 FT DISULFID 33 114 (BY SIMILARITY)
 FT DISULFID 66 71 BY SIMILARITY
 FT DISULFID 120 322 BY SIMILARITY
 FT DISULFID 199 233 BY SIMILARITY
 FT MDL RES 23 23 HYPOTHETICAL Cysteine ACTD
 FT MDL RES 23 23 (BY SIMILARITY)
 SQ SEQUENCE 228 AA 228 AA P05520 CPO32

Query Match 84.8% Score 28; DB 8; Length 328;
 Best Local Similarity 71.4% Pred. No. 97;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0

QY 1 FKLLKK 7
 DB 258 FKLLKK 264

RESULT 14
 ID 081761 PRELIMINARY: PRT: 343 AA
 AC 081761
 DI 01-NOV-1998 (IREMREL. 08. CREATED)
 DI 01-NOV-1998 (IREMREL. 08. LAST SEQUENCE UPDATE)
 DI 01-NOV-1998 (IREMREL. 08. LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL 35.1 KD PROTEIN.
 GN F1715.120.
 OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
 OC EUCARYOTA; EUPHYCOPHYTES; CHAROPHYTES; EMNEMPHYTES;
 OC FRANKELIA; EUPHYCOPHYTES; SPERMATOPHYTES; MAGNOLIOPHYTES;
 OC EUDICOTYLEDONS; ROSIDAE; CAPPARIDAE; BRASSICACEAE; ARABIDOPSIS.
 RN (1)
 RA VITAMIN D 11-HYDROXYLASE, ARABIDOPSIS, DE SIMONE V., HOEISEL J.,
 RA JESSE T., HEINEN L., VOS P., MEMMS H.W., MAYER K.F.X., SCHRELLER C.,
 RA BEVAN M.,
 RL SCREWTER, G. (1998) IN: ENZYME/GENBANK/TOBJ DATA BANKS.
 RN (2)
 RP SEQUENCE FROM N.A.
 RA EU ARABIDOPSIS SEQUENCING PROJECT;
 RI SUBMITTED (1998-1998) TO EMBL/GENBANK/TOBJ DATA BANKS.
 DR EMBL: A031033; E1310395;
 KM HYPOTHETICAL PROTEIN
 SQ SEQUENCE 343 AA; 36104 MW; 0F52C3E9 CPO32;

Query Match 84.8% Score 28; DB 8; Length 343;
 Best Local Similarity 71.4% Pred. No. 10402;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FKLLKK 7
 DB 306 FKLLKK 312

RESULT 15
 ID P72902 PRELIMINARY: PRT: 401 AA.
 AC P72902
 DI 01-FEB-1997 (IREMREL. 02. CREATED)
 DI 01-FEB-1997 (IREMREL. 02. LAST SEQUENCE UPDATE)
 DI 01-NOV-1998 (IREMREL. 08. LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL 46.0 KD PROTEIN.
 OS SYNECHOCYSTIS SP. (STRAIN PCC 6803).
 OC BACTERIA; CYANOBACTERIA; CHROCOCCALES; SYNECHOCYSTIS.
 RN (1)
 RP SEQUENCE FROM N.A.
 RA TABATA S.;

RI SCREWTER, G. (1998) IN: ENZYME/GENBANK/TOBJ DATA BANKS.
 RN (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 97061201.
 RA KANEKO T., SATO S., KOTANI H., TANNO A., ASAYAN F., YAMAMURA Y.,
 RA MIYATAWA N., HIRASAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
 RA HOSOGUCHI T., MATSUNO A., MIYAKI A., NAKAZAKI N., NAKANO K., OKUMURA S.,
 RA SHIMO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,
 RA TABATA S.;
 FT Synchocystis sp. strain PCC6803. II. Sequence determination of the
 FT cldA gene and identification of potential protein coding regions.
 RI DNA RES. 3:109-136(1998).
 DR EMBL: D009034; G1651992;
 DR FRANK: P000534; Glycosyltransferase 1;
 KM HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 401 AA; 40450 MW; B0C0C022 CPO32;

Query Match 84.8% Score 28; DB 9; Length 401;
 Best Local Similarity 71.4% Pred. No. 12042;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FKLLKK 7
 DB 138 FKLLKK 145

Search completed: Jun 23, 1999, 11:01:02
 Job time: 168 sec




```

DE Human interferon inducible protein-1 (HIF-1) [protein]
EN Interferon-inducible protein 1 (IFI-1) [protein]
KW anti-neoplastic, antitubercular, immunomodulator, adaptive immunotherapy,
OS Homo sapiens.
PM Key Location/Qualifiers
PI P04968 1..35
ET /label= leader_peptide
FT 37..193
FI misc_difference 109
FI /label= Mal-protein
FI EF_119031.A2
PM 22-MAY-1996.
PF 10-NOV-1995: 308055.
PR 15-NOV-1994: JP-304203.
BR 24-FEB-1995: JP-058740.
PR 10-MAR-1995: JP-078357.
PR 16-SEP-1995: JP-078952.
PR 23-SEP-1995: JP-274988.
PA (HAVE ) HAYASHIYAMA SEIMITSU KAKUKI.
PI Furuya S., Kobayashi Y., Yoshida T., Kawamoto M., Yamura H.,
PI Taniguchi M., Tomimatsu T., Takahara K., Oshio S.,
DB WPI/JapanBioresourceProject
DR NPJSDB: I52404.
PI ENK (enhancer) located at 1p34.3 in "inducing poly(ADP-ribose)" useful
PI to treat and prevent, e.g viral disease, malignancies and immune
PI disorders.
FS Claim 6: Page 41-42; 48pp; English.
CC The nucleic portion of a novel human protein (P84560) induces IT
CC interferon-gamma (IFN-gamma) produ by immunocompetent cells. It
CC is the product of a cDNA clone (772404) obt'd from a human liver
CC library. The protein enhances the cytotoxicity of killer cells
CC and/or induces the formation of killer cells (e.g NK cells),
CC lymphokine-activating killer (LAK) cells, and cytotoxic T-cells).
CC The mature protein (see also p84560) is useful as an antiviral,
CC anticancer, antibacterial, immunoregulatory and blood platelet
CC enhancing agent, and can be used in adoptive immunotherapy. It is
CC also used to raise monoclonal antibodies.
SQ Seq-viewer 193 AA)

Query Model 100.0% score 27 LB L length 193:
Best model similarity 100.0% Prog No. 20:
Matching 0 Consistency 0 Missed bases 0 Indels 0 Gaps 0

CY 1 MYKDS 5
   1111
DB R7 MYKDS 41

RESULT 4
R07280 standard F1-Lin 606 AA
AC R07280
DI 30-JAN-1997 (first entry)
DE Helicobacter-specific AtPase 430
OE Helicobacter pylori AtPase; model; screening; metabolism.
OS Helicobacter pylori
PN W09617066-A1.
PR 06-JUN-1996.
PR 30-NOV-1996: E74711
PR 02-DEC-1994: U4 44709
PR 18-FEB-1995: E82004AT
EA (BYKS.) BYX GUIDEN LOWBERG CHEM PH.B.
PI Wertheimer R., Schaefer KF., Steinhilber W., Weitzenecker T.;
PI WPI: 96-096981/79.
DB N-RSDB: 128350.
PI Model for screening opds. for inhibition of Helicobacter - is
PI recombinant cell transfected with gene for Helicobacter P-type
PI AtPase under control of inducible promoter
PS Disclature: Fig 2, 7Fig. German.
PI Helicobacter-specific AtPase-gene, 430, 514 and 548 are given
```

```

01 10 1979-1983 and 1983-1985. These pages are reprocessed in
02 1983-1985. When inserted into the 1983-1985 issue
03 a significant change in metabolism.
04 Sequence 686 AA:
05
06
07
08
09
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1
```


Query Match: 100.0% Score 27, DB 1, Length 203.
 Best Local Similarity: 100.0% Pred. No. 21:
 Matches: 5 Conservative 0 Mismatches 0 Indels 0 Gaps 0

Query: 1 MYKUS 5
 11111
 DB: 83 MYKUS 87

Result 13
 W06108 standard: Protein: 203 AA

AC W06108
 DE 01-FEB-1997 (first entry)
 DE Fetal myelin basic protein MBP-X2Cys81/bact.
 KM Myelin basic protein, MBP-X2Cys81, proteolipid protein; PLP.
 KM Multiple sclerosis; autoimmune disease; diagnosis; therapy;
 KM Tryptophan, Tryptophan, Tryptophan, Tryptophan.
 OS Synthesis.
 FH Fetus.
 FT region
 FT 50-85
 FT /note="hexa-histidine tag
 FT /note="exon 2-encoded region, with Cys81ser
 FT mutation"
 FT 196..203
 FT peptide
 FT /label="Hexa-histidine-tag
 FT /note="The hexa-histidine tag facilitates
 FT purification of the recombinant protein
 FT from host cells"

PN W0634622-A1.
 PD 07-NOV-1996:
 PE 22-APR-1996: 005611.
 PR 02-MAY-1995: 05-431644.
 PR 02-MAY-1995: 05-431644.
 PR 07-JUN-1996: 05-482114.
 PA (ALX-1) ALPHAXON PHARM INC
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES
 PI Lemaire MD, Marie L, McFarland HP, Mueller EE, Mueller JP,
 PI Nye SH, Pelletier CM, Squinto SP, Wilkins JA
 PI WP: 96-505896/50.
 DR NIDDK: 14136.
 PT New human myelin basic protein and proteolipid protein variant(s) -
 PT used in the assessment, diagnosis and treatment of multiple
 PT sclerosis

PS Disclosure: Page 81-82: 156pp; English.
 CC A 21.5 kDa foetal isoform (W06107) of myelin basic protein,
 CC MBP-X2Cys81/bact., is the product of a DNA construct (T41946)
 CC based on the human foetal MBP-X2Cys81 isoform (W00399) but
 CC utilizing bacterially-preferred codons in place of the native human
 CC codons (see also T41893). This increases prodn. of the MBP in E.
 CC coli by at least 100%. Recombinant MBP 21.5 polypeptides (see also
 CC W06109 and W06108) are useful in the clinical assessment, diagnosis
 CC and treatment of MS.
 SQ Sequence 203 AA:

Query Match: 100.0% Score 27, DB 1, Length 203.
 Best Local Similarity: 100.0% Pred. No. 21:
 Matches: 5 Conservative 0 Mismatches 0 Indels 0 Gaps 0

Query: 1 MYKUS 5
 11111
 DB: 83 MYKUS 87

Result 13
 W06108 standard: Protein: 203 AA

AC W06108
 DE 01-FEB-1997 (first entry)
 DE Fetal myelin basic protein MBP-X2Cys81/bact.
 KM Myelin basic protein, MBP-X2Cys81, proteolipid protein; PLP.
 KM Multiple sclerosis; autoimmune disease; diagnosis; therapy;
 KM Tryptophan, Tryptophan, Tryptophan, Tryptophan.
 OS Synthesis.
 FH Fetus.
 FT region
 FT 50-85
 FT /note="hexa-histidine tag
 FT /note="exon 2-encoded region, with Cys81ser
 FT mutation"
 FT 196..203
 FT peptide
 FT /label="Hexa-histidine-tag
 FT /note="The hexa-histidine tag facilitates
 FT purification of the recombinant protein
 FT from host cells"

PN W0634622-A1.
 PD 07-NOV-1996:
 PE 22-APR-1996: 005611.
 PR 02-MAY-1995: 05-431644.
 PR 02-MAY-1995: 05-431644.
 PR 07-JUN-1996: 05-482114.
 PA (ALX-1) ALPHAXON PHARM INC
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES
 PI Lemaire MD, Marie L, McFarland HP, Mueller EE, Mueller JP,
 PI Nye SH, Pelletier CM, Squinto SP, Wilkins JA
 PI WP: 96-505896/50.
 DR NIDDK: 14136.
 PT New human myelin basic protein and proteolipid protein variant(s) -
 PT used in the assessment, diagnosis and treatment of multiple
 PT sclerosis

Query Match: 100.0% Score 27, DB 1, Length 203.
 Best Local Similarity: 100.0% Pred. No. 21:
 Matches: 5 Conservative 0 Mismatches 0 Indels 0 Gaps 0

Query: 1 MYKUS 5
 11111
 DB: 83 MYKUS 87

Result 14
 W24262 standard: Protein: 157 AA.

AC W24262
 DE 15-OCT-1997 (first entry)
 DE Murine protein for induction of interferon-gamma.
 KM Interferon-gamma, immunocompetent cell, malignant tumour;
 KM Viral disease; bacterial infection; immune disease.
 OS Mus musculus.
 FH Key
 FT misc_difference 70
 FT /note="Encoded by AYT"

PN J09157180-A.
 PD 17-JUN-1997:
 PE 24-JAN-1996: 028722.
 PR 04-OCT-1995: JP-279906.
 PR 10-MAR-1995: JP-078357.
 PR 29-SEP-1995: JP-074998.
 PA (HABR) HAYASHIBARA SEIROTSU KAKAKU.
 TR WP: 97-46949/34.
 DR N-PSDB: T80210.
 FT A dig containing a poly-peptide which induces interferon-gamma -
 FT useful for treating e.g. malignant tumours, viral, bacterial or
 FT immune diseases

PS Disclosure: Page 10-11, 12pp, Japanese.
 CC This sequence represents a protein which induces interferon-gamma
 CC production in immunocompetent cells. This protein may be used as
 CC the major component in a drug for the prevention and treatment of
 CC e.g. malignant tumours, viral diseases, bacterial infections and
 CC immune diseases.
 SQ Sequence 157 AA:

Query Match: 100.0% Score 27, DB 1, Length 157.
 Best Local Similarity: 100.0% Pred. No. 16:
 Matches: 5 Conservative 0 Mismatches 0 Indels 0 Gaps 0

Query: 1 MYKUS 5
 11111
 DB: 50 MYKUS 54

Result 15
 W24258 standard: Protein: 157 AA.

AC W24258
 DE 15-OCT-1997 (first entry)
 DE Human protein for induction of interferon-gamma.
 KM Interferon-gamma, immunocompetent cell; malignant tumour;
 KM Viral disease; bacterial infection; immune disease.
 OS Homo sapiens.

11 MYKOS 11W

Result 1

Accession: S30945

Molecule type: DNA

Residues: 1-635 <TID>

Cross-references: EMBL: M96847; NID: 914397; PDB: 1A3996

Keywords: ATP, molecular chaperone

Query Match

Best Local Similarity: 100.0%; Pred. No. 53

Matches: 53 Conservative 0 Mismatches 0 Indels 0 Gaps 0

1 MYKOS 5

DB 597 MYKOS 601

Result 6

Accession: G64618

Molecule type: DNA

Residues: 1-688 <TID>

Cross-references: EMBL: M96847; NID: 914397; PDB: 1A3996

Keywords: ATP, molecular chaperone

Query Match

Best Local Similarity: 100.0%; Pred. No. 53

Matches: 53 Conservative 0 Mismatches 0 Indels 0 Gaps 0

1 MYKOS 5

DB 597 MYKOS 601

Result 7

Accession: S38143

Molecule type: DNA

Residues: 1-743 <TID>

Cross-references: EMBL: M96847; NID: 914397; PDB: 1A3996

Keywords: ATP, molecular chaperone

Query Match

Best Local Similarity: 100.0%; Pred. No. 53

Matches: 53 Conservative 0 Mismatches 0 Indels 0 Gaps 0

1 MYKOS 5

DB 597 MYKOS 601

Result 8

Accession: S38143

Molecule type: DNA

Residues: 1-743 <TID>

Cross-references: EMBL: M96847; NID: 914397; PDB: 1A3996

Keywords: ATP, molecular chaperone

Query Match

Best Local Similarity: 100.0%; Pred. No. 53

Matches: 53 Conservative 0 Mismatches 0 Indels 0 Gaps 0

1 MYKOS 5

DB 597 MYKOS 601

Result 9

Accession: S38143

Molecule type: DNA

Residues: 1-743 <TID>

Cross-references: EMBL: M96847; NID: 914397; PDB: 1A3996

Keywords: ATP, molecular chaperone

Query Match

Best Local Similarity: 100.0%; Pred. No. 53

Matches: 53 Conservative 0 Mismatches 0 Indels 0 Gaps 0

1 MYKOS 5

DB 597 MYKOS 601

Result 10

Accession: S38143

Molecule type: DNA

Residues: 1-743 <TID>

Cross-references: EMBL: M96847; NID: 914397; PDB: 1A3996

Keywords: ATP, molecular chaperone

Query Match

Best Local Similarity: 100.0%; Pred. No. 53

Matches: 53 Conservative 0 Mismatches 0 Indels 0 Gaps 0

1 MYKOS 5

DB 597 MYKOS 601

Accession: S30944

Molecule type: DNA

Residues: 1-635 <TID>

Cross-references: EMBL: M96847; NID: 914397; PDB: 1A3996

Keywords: ATP, molecular chaperone

Query Match

Best Local Similarity: 100.0%; Pred. No. 53

Matches: 53 Conservative 0 Mismatches 0 Indels 0 Gaps 0

1 MYKOS 5

DB 597 MYKOS 601

Result 6

Accession: G64618

Molecule type: DNA

Residues: 1-688 <TID>

Cross-references: EMBL: M96847; NID: 914397; PDB: 1A3996

Keywords: ATP, molecular chaperone

Query Match

Best Local Similarity: 100.0%; Pred. No. 53

Matches: 53 Conservative 0 Mismatches 0 Indels 0 Gaps 0

1 MYKOS 5

DB 597 MYKOS 601

Result 7

Accession: S38143

Molecule type: DNA

Residues: 1-743 <TID>

Cross-references: EMBL: M96847; NID: 914397; PDB: 1A3996

Keywords: ATP, molecular chaperone

Query Match

Best Local Similarity: 100.0%; Pred. No. 53

Matches: 53 Conservative 0 Mismatches 0 Indels 0 Gaps 0

1 MYKOS 5

DB 597 MYKOS 601

Result 8

Accession: S38143

Molecule type: DNA

Residues: 1-743 <TID>

Cross-references: EMBL: M96847; NID: 914397; PDB: 1A3996

Keywords: ATP, molecular chaperone

Query Match

Best Local Similarity: 100.0%; Pred. No. 53

Matches: 53 Conservative 0 Mismatches 0 Indels 0 Gaps 0

1 MYKOS 5

DB 597 MYKOS 601

Result 9

Accession: S38143

Molecule type: DNA

Residues: 1-743 <TID>

Cross-references: EMBL: M96847; NID: 914397; PDB: 1A3996

Keywords: ATP, molecular chaperone

Query Match

Best Local Similarity: 100.0%; Pred. No. 53

Matches: 53 Conservative 0 Mismatches 0 Indels 0 Gaps 0

1 MYKOS 5

DB 597 MYKOS 601

Result 10

Accession: S38143

Molecule type: DNA

Residues: 1-743 <TID>

Cross-references: EMBL: M96847; NID: 914397; PDB: 1A3996

Keywords: ATP, molecular chaperone

Query Match

Best Local Similarity: 100.0%; Pred. No. 53

Matches: 53 Conservative 0 Mismatches 0 Indels 0 Gaps 0

1 MYKOS 5

DB 597 MYKOS 601

C:Genetics:
A:MAP position: 11E
C:Keywords: transmembrane protein

Query Match 88 94 Score 24 DB 2 Length 511
Best local similarity 100 0% Prod No 37402
Matches 4: Conservative 0 Mismatches 0 Indels 0 Gaps 0

Cy 1 MYKDS 5
DB 329 MYKDS 722

RESULT 8
S60224
C:Sequence: 101F - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Apr-1994 #sequence_revision 19-Apr-1996 #text_change 10-Sep-1997
C:Accession: S60226
R:Okamura, H.; Yutsudo, H.; Komatsu, T.; Yutsudo, M.; Hakura, A.; Tanimoto, T.; Toriue,
Nature 378, 88-91, 1995
A:Title: Cloning of a new cytokine that induces IFN-gamma production by T cells.
A:Reference number: S60226
A:Accession: S60226
A>Status: Preliminary
A:Molecule type: mRNA
A:Peptides: 1192 (OKKA)
A:Cross-references: EMBL:U00419 NID:91064822 PIR:J100319 PIR:91064822

Query Match 100 0% Score 27 DB 2 Length 193
Best local similarity 100 0% Prod No 151
Matches 5: Conservative 0 Mismatches 0 Indels 0 Gaps 0

Cy 1 MYKDS 5
DB 85 MYKDS 43

RESULT 9
XND00
C:Sequence: 1-phosphate uridylyltransferase (EC 2.7.7.9) - slime mold (Dictyostellium di-
C:Species: Dictyostellium discoideum
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 08-Sep-1997
C:Accession: S07863
R:Radheh, J.A.; Dettin, R.P.
Nucleic Acids Res 15, 3841-3846, 1987
A:Title: Structure and sequence of a HCF glucose pyrophosphorylase gene of Dictyostellium
A:Reference number: S07863 MIM:67211075
A:Accession: S07863
A:Molecule type: DNA
A:Peptides: 1311 (KAG)
A:Cross-references: EMBL:Y00145 NID:97384 PIR:97385
C:Comments: This enzyme catalyzes alpha-D-glucose-1-phosphate and nucleoside triphosphate
C:Genetics:
A:Introns: 1671-1711 bp
A:Superfamily: uridylyltransferase
C:Keywords: nucleotidyltransferase

Query Match 88 94 Score 24 DB 1 Length 511
Best local similarity 80 0% Prod No 37402
Matches 4: Conservative 1 Mismatches 0 Indels 0 Gaps 0

Cy 1 MYKDS 5
DB 200 MYKDS 212
RESULT 10

A24050
C:Sequence: ribonucleoside-diphosphate reductase (EC 1.17.4.1) chain M - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Jul-1987 #sequence_revision 06-Jul-1987 #text_change 19-Jun-1993
C:Accession: A24050
R:Baras, I.W.; Levinson, P.B.; Brady, M.; Williams, S.R.; Martin D.W.; D.W.
J. Biol. Chem. 262, 3413-3420, 1987
A:Reference number: A24050 MIM:60240721
A:Accession: A24050
A:Molecule type: mRNA
A:Peptides: 1792 (CAR)
C:Superfamily: herpervirus ribonucleoside-diphosphate reductase large chain
C:Keywords: DNA replication, oxidoreductase

Query Match 88 94 Score 24 DB 2 Length 722
Best local similarity 80 0% Prod No 37402
Matches 4: Conservative 1 Mismatches 0 Indels 0 Gaps 0

Cy 1 MYKDS 5
DB 406 LYKDS 410

RESULT 11
S14807
C:Sequence: ribonucleoside-diphosphate reductase (EC 1.17.4.1) large chain - fission yeast (Schiz-
C:Species: Schizosaccharomyces pombe
C:Date: 31-Dec-1994 #sequence_revision 11-Dec-1994 #text_change 15-Sep-1997
C:Accession: S14807
R:Sarabia, M.J.F.; McInerney, C.; Harris, P.; Gordon, C.; Fantes, P.
Mol. Gen. Genet. 229, 241-251, 1993
A:Title: The cell cycle clock, cell cycle, and evolution of the fission yeast Schizosaccha-
A:Reference number: S14807
A:Accession: S14807
A:Molecule type: DNA
A:Peptides: 1811 (SAR)
A:Cross-references: EMBL:X67110 NID:9277445 PIR:9277447
C:Genetics:
A:Gene: cdc22
A:Introns: 7/1
C:Superfamily: herpervirus ribonucleoside-diphosphate reductase large chain
C:Keywords: DNA replication, oxidoreductase

Query Match 88 94 Score 24 DB 2 Length 511
Best local similarity 80 0% Prod No 37402
Matches 4: Conservative 1 Mismatches 0 Indels 0 Gaps 0

Cy 1 MYKDS 5
DB 400 LYKDS 410

RESULT 12
B48687
C:Sequence: ribonucleoside-diphosphate reductase (EC 1.17.4.1) large chain - plasmodium falciparum
C:Species: Plasmodium falciparum
C:Date: 09-May-1994 #sequence_revision 13-May-1994 #text_change 21-May-1995
C:Accession: B48687
R:Roblin, H.; Salem, D.S.; Li, L.S.; Yang, F.; Muma, S.; Ward, L.; Fisher, A.; Bannan,
Proc. Natl. Acad. Sci. U.S.A. 90, 9480-9484, 1993
A:Title: Cloning, sequence determination, and regulation of the ribonucleotide reduct-
A:Reference number: A48687
A:Accession: B48687
A>Status: Preliminary
A:Molecule type: DNA
A:Peptides: 1804 (RCE)
A:Cross-references: EMBL:U00419 NID:9319731 PIR:9319702
C:Superfamily: herpervirus ribonucleoside-diphosphate reductase large chain
C:Keywords: herpervirus, ribonucleoside-diphosphate reductase, cell cycle, cell cycle, cell cycle
R:17-443 700-802/Chromatid bands recombination status predicted
R:427-429/Active site Asp 316 status predicted

Bacillus subtilis

ALIGNMENTS

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
84

JOHN A. ...

2341
 2342
 2343
 2344
 2345
 2346
 2347
 2348
 2349
 2350
 2351
 2352
 2353
 2354
 2355
 2356
 2357
 2358
 2359
 2360
 2361
 2362
 2363
 2364
 2365
 2366
 2367
 2368
 2369
 2370
 2371
 2372
 2373
 2374
 2375
 2376
 2377
 2378
 2379
 2380
 2381
 2382
 2383
 2384
 2385
 2386
 2387
 2388
 2389
 2390
 2391
 2392
 2393
 2394
 2395
 2396
 2397
 2398
 2399
 2400
 2401
 2402
 2403
 2404
 2405
 2406
 2407
 2408
 2409
 2410
 2411
 2412
 2413
 2414
 2415
 2416
 2417
 2418
 2419
 2420
 2421
 2422
 2423
 2424
 2425
 2426
 2427
 2428
 2429
 2430
 2431
 2432
 2433
 2434
 2435
 2436
 2437
 2438
 2439
 2440
 2441
 2442
 2443
 2444
 2445
 2446
 2447
 2448
 2449
 2450
 2451
 2452
 2453
 2454
 2455
 2456
 2457
 2458
 2459
 2460
 2461
 2462
 2463
 2464
 2465
 2466
 2467
 2468
 2469
 2470
 2471
 2472
 2473
 2474
 2475
 2476
 2477
 2478
 2479
 2480
 2481
 2482
 2483
 2484
 2485
 2486
 2487
 2488
 2489
 2490
 2491
 2492
 2493
 2494
 2495
 2496
 2497
 2498
 2499
 2500
 2501
 2502
 2503
 2504
 2505
 2506
 2507
 2508
 2509
 2510
 2511
 2512
 2513
 2514
 2515
 2516
 2517
 2518
 2519
 2520
 2521
 2522
 2523
 2524
 2525
 2526
 2527
 2528
 2529
 2530
 2531
 2532
 2533
 2534
 2535
 2536
 2537
 2538
 2539
 2540
 2541
 2542
 2543
 2544
 2545
 2546
 2547
 2548
 2549
 2550
 2551
 2552
 2553
 2554
 2555
 2556
 2557
 2558
 2559
 2560
 2561
 2562
 2563
 2564
 2565
 2566
 2567
 2568
 2569
 2570
 2571
 2572
 2573
 2574
 2575
 2576
 2577
 2578
 2579
 2580
 2581
 2582
 2583
 2584
 2585
 2586
 2587
 2588
 2589
 2590
 2591
 2592
 2593
 2594
 2595
 2596
 2597
 2598
 2599
 2600
 2601
 2602
 2603
 2604
 2605
 2606
 2607
 2608
 2609
 2610
 2611
 2612
 2613
 2614
 2615
 2616
 2617
 2618
 2619
 2620
 2621
 2622
 2623
 2624
 2625
 2626
 2627
 2628
 2629
 2630
 2631
 2632
 2633
 2634
 2635
 2636
 2637
 2638
 2639
 2640
 2641
 2642
 2643
 2644
 2645
 2646
 2647
 2648
 2649
 2650
 2651
 2652
 2653
 2654
 2655
 2656
 2657
 2658
 2659
 2660
 2661
 2662
 2663
 2664
 2665
 2666
 2667
 2668
 2669
 2670
 2671
 2672
 2673
 2674
 2675
 2676
 2677
 2678
 2679
 2680
 2681
 2682
 2683
 2684
 2685
 2686
 2687
 2688
 2689
 2690
 2691
 2692
 2693
 2694
 2695
 2696
 2697
 2698
 2699
 2700
 2701
 2702
 2703
 2704
 2705
 2706
 2707
 2708
 2709
 2710
 2711
 2712
 2713
 2714
 2715
 2716
 2717
 2718
 2719
 2720
 2721
 2722
 2723
 2724
 2725
 2726
 2727
 2728
 2729
 2730
 2731
 2732
 2733
 2734
 2735
 2736
 2737
 2738
 2739
 2740
 2741
 2742
 2743
 2744
 2745
 2746
 2747
 2748
 2749
 2750
 2751
 2752
 2753
 2754
 2755
 2756
 2757
 2758
 2759
 2760
 2761
 2762
 2763
 2764
 2765
 2766
 2767
 2768
 2769
 2770
 2771
 2772
 2773
 2774
 2775
 2776
 2777
 2778
 2779
 2780
 2781
 2782
 2783
 2784
 2785
 2786
 2787
 2788
 2789
 2790
 2791
 2792
 2793
 2794
 2795

30 REFERENCE 133 AA 20326 MW 7855717 CDS20

Query Match 100.0% Score 27, FR 1, Length 193
Best Local Similarity 100.0% Pred. No. 9
Matches 5: Conservative 0, Mismatches 0, Indels 0, Gaps 0

OY 1 MYKDS 5
1111
DB 87 MYKDS 21

RESULT 5
ID IL18_MOUSE
AC P30380
DI 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DI 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DI 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE INTERLEUKIN-18 PROTEIN (IL-18) (INTERFERON-GAMMA INDUCING FACTOR)
DE (IFN-GAMMA-INDUCING FACTOR) (INTERLEUKIN-1 GAMMA) (IL-1 GAMMA)
GN IL18 OR IL18F
OS MUS MUSCULUS (MOUSE)
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC EUHERPETA: RODENTIA:
RN (1)
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RX TISSUE=LIVER
RC MEDLINE: 96061009
RA KANAKURA H., ISHIGURO H., KOMATSU I., YOTSUDO M., HANUKA A.,
RA TANIMOTO T., TORIGOE K., OKURA I., NAKADA Y., HATTORI K.,
RA AITA R., NAKAMA M., TANAKA F., KINISHI K., FUKUDA S., KITAMOTO M.,
RN 121
RE NATURE 378:80-91(1992).
RF SEQUENCE OF 1-121 FROM N.A.
RC STRAIN=NO. 11556-PANCREAS;
RX MEDLINE: 97774346
RA FORTIN F., TREMBIN R.A., COPELAND N.G., KOLP H
RL J. CLIN. INVEST. 99:469-474(1997).
CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE 1
CC CELLS.
DE EMBL: 049449; GI044923; 1
DR EMBL: 066244; GI561786; 1
DF MEG. M31 107256 181F
KW CYTOKINE
FT PROPEP 1 35
FT CHAIN 36 192 INTERLEUKIN-18
FT CONFID 188 192 NOT IN (IN REF 2)
SC SEQUENCE 193 AA 20326 MW 4939799 CDS20

Query Match 100.0% Score 27, DB 1, Length 192
Best Local Similarity 100.0% Pred. No. 8.5
Matches 5: Conservative 0, Mismatches 0, Indels 0, Gaps 0

OY 1 MYKDS 5
1111
DB 85 MYKDS 89

RESULT 5
ID IL18_PIG
AC 019073
DI 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DI 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DI 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE INTERLEUKIN-18 PROTEIN (IL-18) (INTERFERON-GAMMA INDUCING FACTOR)
DE (IFN-GAMMA-INDUCING FACTOR) (INTERLEUKIN-1 GAMMA) (IL-1 GAMMA)
GN IL18 OR IL18F
OS SUS SCR FA (PIG)
SCS SCR FA (PIG)

31 EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC EUHERPETA: ARTIODACTYLA:
RN (1)
RP SEQUENCE FROM N.A.
RA FOSS D.L., MORTAUGH M.P.,
RA SEIBELT D. (JUL-1997) 10 EMBL/GENBANK/CCP DATA BANKS.
CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE 1
CC CELLS (BY SIMILARITY).
DE EMBL: 069791; GI228534; 1
DR EMBL: 069791; GI228534; 1
KW CYTOKINE
FT PROPEP 1 35 BY SIMILARITY.
FT CHAIN 36 160 INTERLEUKIN-18.
FT NONTER 160 160
SC SEQUENCE 194 AA 22363 MW 26100290 CDS22

Query Match 100.0% Score 27, DB 1, Length 190
Best Local Similarity 100.0% Pred. No. 7.3
Matches 5: Conservative 0, Mismatches 0, Indels 0, Gaps 0

OY 1 MYKDS 5
1111
DB 86 MYKDS 90

RESULT 7
ID IL18_RAT
AC P97637
DI 15-JUL-1998 (REL. 36, CREATED)
DI 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DI 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE INTERLEUKIN-18 PROTEIN (IL-18) (INTERFERON-GAMMA INDUCING FACTOR)
DE (IFN-GAMMA-INDUCING FACTOR) (INTERLEUKIN-1 GAMMA) (IL-1 GAMMA)
GN IL18 OR IL18F
OS RATUS NORVEGICUS (RA)
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC EUHERPETA: RODENTIA:
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=ADRENAL GLAND;
RX MEDLINE: 97152963
RA CONTI R., JAHNG J.W., TINTI C., SON J.H., JOH T.H.,
RL J. Biol. Chem. 272:2096-2097(1997).
CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE 1
CC CELLS.
DE EMBL: 077766; GI092129; 1
DR EMBL: 077777; GI092131; 1
FW CYTOKINE: ALTERNATIVE SPLICING.
KW CYTOKINE
FT PROPEP 1 36
FT CHAIN 37 193 BY SIMILARITY.
FT VARSPLIC 121 193 MISSING (IN ISOFORM ALPHA).
SC SEQUENCE 194 AA 22363 MW 78103221 CDS22

Query Match 100.0% Score 27, DB 1, Length 194
Best Local Similarity 100.0% Pred. No. 9
Matches 5: Conservative 0, Mismatches 0, Indels 0, Gaps 0

OY 1 MYKDS 5
1111
DB 87 MYKDS 91

RESULT 8
ID MBP_HUMAN
AC P02080
DI 21-JUL-1998 (REL. 01, CREATED)
DI 01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
DI 01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)

```

FT FT DOMAIN: 43 114 INDOCS, EXPERIMENTAL, APOURININE
FT FT AND PATS BUT NOT IN OTHER PDS.
FT FT DOMAIN 138 148 INDOCS, EXPERIMENTAL, APOURININE
FT FT VARSELIC 59 84 ENCEPHALOMYELITIS.
FT FT VARSELIC 132 142 MISSING (IN 18.5 KD FORM AND 17.2 KD
SC SEQUENCE 196 AA: 21462 MW: 0A8564EE CRC32: FORM).

Query Match: 100.0%; Score 27; DB 1; Length 196;
Best Local Similarity: 100.0%; Pct. No. 1;
Matches: 5; Conservative: 0; Mismatches: 0; Indels: 0; Gaps:

OY 1 MYKDS 5
DB 82 MYKDS 86

RESULT 9
MBP_MOUSE
ID MBP_MOUSE STANDARD: PRT: 194 AA.
AC P04370;
DT 20-MAR-1987 (REL. 04, CREATED)
E1 01-JAN-1984 (REL. 06, LAST SEQUENCE UPDATE)
D1 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE MYELIN BASIC PROTEIN (MBP).
GN MBP.
OS MUS MUSCULUS (MOUSE).
OC ERYTHROCYTE METAZOAN; CHEMIDIA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; MAMMALIA.
RN (1)
RA RP SEQUENCE FROM N.A. (ALL FOUR FORMS).
RX MEDLINE: 86079555.
RA FE PERPA F., ENCH H., HUSON L., KAMHOLZ J., PUKELL J., WILKINSON S.,
RA LAZZARINI R.A.;
RL CELL 43:723-727(1985).
RN (2)
RA RP SEQUENCE FROM N.A. (18.5 KD FORM).
RX MEDLINE: 85254913.
RA TAKAHASHI N., ROACH A., TEFLOW D.B., PROSINER S.R., H. T. L.;
RL CELL 42:139-148(1985).
RN (3)
RA RP SEQUENCE FROM N.A. (17 KD FORM).
RX MEDLINE: 87118269.
RA NEWMAN S., KITAMURA K., CAMPAGNONI A.T.;
RL PROC NATL ACAD SCI U S A 84:886-890(1987).
RN (4)
RA RP SEQUENCE OF 1-23 FROM N.A.
RX MEDLINE: 89252919.
RA KIDWA M., TAMURA T.A., AOYAMA A., MIKOSHIBA K.;
RL GENE 75:31-38(1989).
OC CC -1- FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN PROPER STRUCTURE
OF MYELIN.
OC CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYELIN.
OC CC -1- ALTERNATIVE PRODUCTS: MOUSE HAS FOUR FORMS OF MBP, 21.5KD, 18.5KD,
17KD, AND 14KD, PRESENT IN RELATIVE AMOUNTS OF 1:10:3:5.183. THE SE
4 FORMS ARE PRODUCED BY ALTERNATIVE SPLICING.
OC CC -1- THE SEQUENCE SHOWN IS THAT OF THE 21.5KD FORM.
OR EMBL: M1553; G387414; JOINED.
OR EMBL: M1291; G387414; JOINED.
OR EMBL: M1529; G387414; JOINED.
OR EMBL: M1550; G387414; JOINED.
OR EMBL: M1551; G387414; JOINED.
OR EMBL: M1552; G387414; JOINED.
OR EMBL: M1553; G387415; JOINED.
OR EMBL: M1554; G387415; JOINED.
OR EMBL: M1555; G387415; JOINED.
OR EMBL: M1556; G387415; JOINED.
OR EMBL: M1557; G387415; JOINED.
OR EMBL: M1558; G387415; JOINED.
OR EMBL: M1559; G387415; JOINED.
OR EMBL: M1560; G387415; JOINED.
OR EMBL: M1561; G387415; JOINED.
OR EMBL: M1562; G387415; JOINED.
OR EMBL: M1563; G387415; JOINED.
OR EMBL: M1564; G387415; JOINED.
OR EMBL: M1565; G387415; JOINED.
OR EMBL: M1566; G387415; JOINED.
OR EMBL: M1567; G387415; JOINED.
OR EMBL: M1568; G387415; JOINED.
OR EMBL: M1569; G387415; JOINED.
OR EMBL: M1570; G387415; JOINED.
OR EMBL: M1571; G387415; JOINED.
OR EMBL: M1572; G387415; JOINED.
OR EMBL: M1573; G387415; JOINED.
OR EMBL: M1574; G387415; JOINED.
OR EMBL: M1575; G387415; JOINED.
OR EMBL: M1576; G387415; JOINED.
OR EMBL: M1577; G387415; JOINED.
OR EMBL: M1578; G387415; JOINED.
OR EMBL: M1579; G387415; JOINED.
OR EMBL: M1580; G387415; JOINED.
OR EMBL: M1581; G387415; JOINED.
OR EMBL: M1582; G387415; JOINED.
OR EMBL: M1583; G387415; JOINED.
OR EMBL: M1584; G387415; JOINED.
OR EMBL: M1585; G387415; JOINED.
OR EMBL: M1586; G387415; JOINED.
OR EMBL: M1587; G387415; JOINED.
OR EMBL: M1588; G387415; JOINED.
OR EMBL: M1589; G387415; JOINED.
OR EMBL: M1590; G387415; JOINED.
OR EMBL: M1591; G387415; JOINED.
OR EMBL: M1592; G387415; JOINED.
OR EMBL: M1593; G387415; JOINED.
OR EMBL: M1594; G387415; JOINED.
OR EMBL: M1595; G387415; JOINED.
OR EMBL: M1596; G387415; JOINED.
OR EMBL: M1597; G387415; JOINED.
OR EMBL: M1598; G387415; JOINED.
OR EMBL: M1599; G387415; JOINED.
OR EMBL: M1600; G387415; JOINED.
OR EMBL: M1601; G387415; JOINED.
OR EMBL: M1602; G387415; JOINED.
OR EMBL: M1603; G387415; JOINED.
OR EMBL: M1604; G387415; JOINED.
OR EMBL: M1605; G387415; JOINED.
OR EMBL: M1606; G387415; JOINED.
OR EMBL: M1607; G387415; JOINED.
OR EMBL: M1608; G387415; JOINED.
OR EMBL: M1609; G387415; JOINED.
OR EMBL: M1610; G387415; JOINED.
OR EMBL: M1611; G387415; JOINED.
OR EMBL: M1612; G387415; JOINED.
OR EMBL: M1613; G387415; JOINED.
OR EMBL: M1614; G387415; JOINED.
OR EMBL: M1615; G387415; JOINED.
OR EMBL: M1616; G387415; JOINED.
OR EMBL: M1617; G387415; JOINED.
OR EMBL: M1618; G387415; JOINED.
OR EMBL: M1619; G387415; JOINED.
OR EMBL: M1620; G387415; JOINED.
OR EMBL: M1621; G387415; JOINED.
OR EMBL: M1622; G387415; JOINED.
OR EMBL: M1623; G387415; JOINED.
OR EMBL: M1624; G387415; JOINED.
OR EMBL: M1625; G387415; JOINED.
OR EMBL: M1626; G387415; JOINED.
OR EMBL: M1627; G387415; JOINED.
OR EMBL: M1628; G387415; JOINED.
OR EMBL: M1629; G387415; JOINED.
OR EMBL: M1630; G387415; JOINED.
OR EMBL: M1631; G387415; JOINED.
OR EMBL: M1632; G387415; JOINED.
OR EMBL: M1633; G387415; JOINED.
OR EMBL: M1634; G387415; JOINED.
OR EMBL: M1635; G387415; JOINED.
OR EMBL: M1636; G387415; JOINED.
OR EMBL: M1637; G387415; JOINED.
OR EMBL: M1638; G387415; JOINED.
OR EMBL: M1639; G387415; JOINED.
OR EMBL: M1640; G387415; JOINED.
OR EMBL: M1641; G387415; JOINED.
OR EMBL: M1642; G387415; JOINED.
OR EMBL: M1643; G387415; JOINED.
OR EMBL: M1644; G387415; JOINED.
OR EMBL: M1645; G387415; JOINED.
OR EMBL: M1646; G387415; JOINED.
OR EMBL: M1647; G387415; JOINED.
OR EMBL: M1648; G387415; JOINED.
OR EMBL: M1649; G387415; JOINED.
OR EMBL: M1650; G387415; JOINED.
OR EMBL: M1651; G387415; JOINED.
OR EMBL: M1652; G387415; JOINED.
OR EMBL: M1653; G387415; JOINED.
OR EMBL: M1654; G387415; JOINED.
OR EMBL: M1655; G387415; JOINED.
OR EMBL: M1656; G387415; JOINED.
OR EMBL: M1657; G387415; JOINED.
OR EMBL: M1658; G387415; JOINED.
OR EMBL: M1659; G387415; JOINED.
OR EMBL: M1660; G387415; JOINED.
OR EMBL: M1661; G387415; JOINED.
OR EMBL: M1662; G387415; JOINED.
OR EMBL: M1663; G387415; JOINED.
OR EMBL: M1664; G387415; JOINED.
OR EMBL: M1665; G387415; JOINED.
OR EMBL: M1666; G387415; JOINED.
OR EMBL: M1667; G387415; JOINED.
OR EMBL: M1668; G387415; JOINED.
OR EMBL: M1669; G387415; JOINED.
OR EMBL: M1670; G387415; JOINED.
OR EMBL: M1671; G387415; JOINED.
OR EMBL: M1672; G387415; JOINED.
OR EMBL: M1673; G387415; JOINED.
OR EMBL: M1674; G387415; JOINED.
OR EMBL: M1675; G387415; JOINED.
OR EMBL: M1676; G387415; JOINED.
OR EMBL: M1677; G387415; JOINED.
OR EMBL: M1678; G387415; JOINED.
OR EMBL: M1679; G387415; JOINED.
OR EMBL: M1680; G387415; JOINED.
OR EMBL: M1681; G387415; JOINED.
OR EMBL: M1682; G387415; JOINED.
OR EMBL: M1683; G387415; JOINED.
OR EMBL: M1684; G38
```


Job time: 71 sec

ATPA_ME1BA
 ID ATPA_ME1BA STANDARD: PRT: 578 AA.
 AC P22662;
 DT 01-AUG-1991 (REL. 19, CREATED)
 DT 01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
 DT 01-MAY-1992 (REL. 22, LAST ANNOTATION UPDATE)
 DE ATP SYNTHASE ALPHA CHAIN (EC 3.6.1.34).
 GN ATPA.
 OS METHANOSARSTINA BARKERI.
 CC ARCHAEBACTERIA: EUBACTERIA: MITOCHONDRIALS: METHANOSARSTINACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 83291829.
 RA YANOWITZ K.L., EYA S., MAEDA M., PUTAI M.;
 RL J. BIOL. CHEM. 264:10954-10959(1989).
 CC THIS IS A CATALYTIC SUBUNIT.
 CC -1- SIMILARITY: STRONG TO OTHER ARCHAEACTERIA ALPHA SUBUNITS, ALSO
 CC RELATED TO THE BETA SUBUNITS OF FO-F1 ATPASES.
 DR EMBL: J04836; G149820; -.
 DR PIR: A34293; A34283.
 DR PROSITE: PS00152: ATPASE ALPHA BETA: 1.
 KW ATP SYNTHESIS; HYDROGEN ION TRANSPORT; HYDROLASE; ATP-BINDING.
 FT M_9IND 228 235 ATP (BY SIMILARITY).
 SQ SEQUENCE 578 AA: 64638 MW: 441647 CPG32;

Query Match 88.9%; Score 24; DB 1; Length 578;
 Best Local Similarity 80.0%; Pred. No. 1.6e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYKDS 5
 DB 430 LYKDS 434

RESULT 15
 ATZC_PSESD
 ID ATZC_PSESD STANDARD: PRT: 403 AA.
 AC 05063;
 DT 15-JUL-1998 (REL. 36, CREATED)
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE N-ISOPROPYLAMMELITE ISOPROPYL AMIDHYDROLASE (EC 3.5.1.-).
 GN ATZC.
 OS PSEUDOMONAS SP. (STRAIN ADP).
 CC PERKARIOTA: SPACILLITICES: SPACILLITICIA: AEROBIC BODS AND CROO2;
 CC PSEUDOMONADACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 38083068.
 RA SADOWSKY M.C., TONG Z., DE SOUZA M., WACKETT L.F.,
 RL J. BACTERIOL. 180:152-158(1998).
 CC FUNCTION: TRANSFORMS N-ISOPROPYLAMMELITE TO CYANURIC ACID AND
 CC ISOPROPYLAMINE.
 CC -1- PATHWAY: THIRD STEP IN AIPALINE DEGRADATION PATHWAY.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
 CC -1- SIMILARITY: RELATIONS TO THE N-ACTYL-D-AMINO-ACID DEACYLASE FAMILY.
 DE EMBL: AF017572; G2735101; -.
 KW HYDROLASE.
 SQ SEQUENCE 403 AA: 41938 MW: 39909281 CPG32;

Query Match 88.9%; Score 24; DB 1; Length 403;
 Best Local Similarity 80.0%; Pred. No. 1.1e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYKDS 5
 DB 267 LYKDS 271

Search completed: June 22, 1999, 10:59:45



PA
FEB 1968
C
C

PA
FEB 1968
C
C

PA TERN S OF TYPING: TAVITT A, ELLMAN L, GARNER D, GEDDI P

DT 01-NOV-1998 (REMEMPHI OR CREATED)
 DT 01-NOV-1998 (REMEMPHI OR LAST SOURCE UPDATE)
 DT 01-NOV-1998 (REMEMPHI OR LAST ANNOTATION UPDATE)
 DE 1103-1 PROTEIN (FRAGMENT).
 GN 1103-1.
 OS APARTHEIDUS ITALIANA (MOUSE-EAR PRESS).
 OT PRAVAYOTA VITAMINATAP, CHAPAPHTA/EMERGEROTA TAPPA, EMERGEROTA
 ICHACHOCHYATA, ECHACHOCHYATA, SEMACHOCHYATA, MACACHOCHYATA,
 CHACHOCHYOTACHONS, MOCHACH, CAPACHAPHTA, RACHACHACHAP, ARACHIDOPHTSIS,
 RN 11)
 RP SOURCE FROM N.A.
 MC STRAIN-CV, COLUMBIA U. 1150E-SILICOES;
 MA ARACHIDUS S.;
 RL THESIS (1998), UNIVERSITE PARIS, FRANCE.
 DR EMBL: A1011845, E1331507; .
 FI NONLIER 1
 FI NONLIER 1
 FI NONLIER 1
 SEQUENCE 44 AA (2007 MS) ANALYTIC SPECIES:
 Query Mail: 82 Gs 839-04 TP 9, 10000, 046;
 Post Local Simulation: 80.0%; Pred No. 1158-00;

Search completed: June 22, 1999, 11:01:23
Job time: 169 sec



GenCore version 4.5
Copyright (c) 1998 Computer Ltd

OM protein - protein search using sw model

Run on: June 22, 1999, 10:58:48 : Search time 61.51 seconds

(without alignments)
3.045 Million cell updates/sec

Title: US-09-030-061-5

Perfect score: 26

Sequence: 1 STISC 5

Scoring table: 2200000

Search: 117738 seqs, 2760011 residues

Database: PIR-S8*

1: p1r1*

2: p1r2*

3: p1r3*

4: p1r4*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Query Match	Length	CP	IT	Description
1	26	100.0	915	1	MMBEV3
2	25	100.0	502	1	UGBCPP
3	24	100.0	784	1	346631
4	24	100.0	32	2	PC2302
5	24	100.0	32	2	PC2302
6	24	100.0	984	2	A29513
7	24	100.0	278	2	A23475
8	24	100.0	302	2	S10420
9	24	100.0	144	2	A48722
10	24	100.0	720	2	A48722
11	24	100.0	337	2	S68678
12	24	100.0	330	2	S17177
13	24	100.0	330	2	A46152
14	24	100.0	113	2	H64148
15	24	100.0	215	2	E71484
16	24	100.0	840	2	S48975
17	24	100.0	104	2	S67404
18	24	100.0	106	2	S69325
19	24	100.0	412	2	S20229
20	24	100.0	400	2	A30350
21	24	100.0	509	2	S43465
22	24	100.0	509	2	A48722
23	24	100.0	182	2	S69326
24	24	100.0	923	1	S47738
25	24	100.0	465	1	S47738
26	24	100.0	1136	1	PFHSCP
27	24	100.0	970	2	164133
28	24	100.0	113	2	S66277
29	24	100.0	113	2	S66277
30	24	100.0	113	2	S66277
31	24	100.0	113	2	S66277
32	24	100.0	113	2	S66277
33	24	100.0	113	2	S66277
34	24	100.0	113	2	S66277
35	24	100.0	113	2	S66277
36	24	100.0	113	2	S66277
37	24	100.0	113	2	S66277
38	24	100.0	113	2	S66277
39	24	100.0	113	2	S66277

40	23	88.5	129	1	K3HMT
41	23	88.5	100	1	K3HMT
42	23	88.5	100	1	K3HMT
43	23	88.5	100	1	K3HMT
44	23	88.5	100	1	K3HMT
45	23	88.5	100	1	K3HMT

ALIGNMENTS

RESULT 1

MMBEV3

ribonucleoside diphosphate reductase (EC 1.17.4.1) large chain - human cytomegalovirus

Alternate names: ribonucleoside reductase large chain, UL15 protein

C-Species: human cytomegalovirus, human herpesvirus 5

A-Note: host Homo sapiens (man)

C-Accession: S09808

C-Accession: S09808

C-Accession: S09808

C-Accession: S09808

C-Accession: S09808

C-Accession: S09808

C-Accession: S09808

C-Accession: S09808

C-Accession: S09808

C-Accession: S09808

C-Accession: S09808

C-Accession: S09808

C-Accession: S09808

C-Accession: S09808

C-Accession: S09808

C-Accession: S09808

C-Accession: S09808

C-Accession: S09808

C-Accession: S09808

C-Accession: S09808

C-Accession: S09808

C-Accession: S09808

C-Accession: S09808

C-Accession: S09808

C-Accession: S09808

C-Accession: S09808

C-Accession: S09808

C-Accession: S09808

A:Molecule type: mRNA
 A:Residues: 1-964 <ASP>
 A:Cross-references: 158 MISC01, NID:947850, PID:9407166
 C:Genetics:
 A:Gene: gfp-MIP
 A:Map position: 4331-4491
 A:Map position: 4331-4491
 C:Superfamily: unassigned eta-related proteins; eta transforming protein homology
 C:Keywords: DNA binding, transcription regulation, zinc finger
 F:661-680/Domain: eta transforming protein homology <EMBL>
 F:681-721/Domain: eta finger
 F:722-964/Domain: zinc finger

Query Match: 100.0%, Score 26, DB 2, Length 984,
 Best Local Similarity: 100.0%, Prod No. 25002,
 Matches 5, Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 1 STISC 5
 Db 152 STISC 156

RESULT 7
 A23475
 G surface protein - Parametium primurella (SGCS)
 C:Species: Parametium primurella
 C:Date: 31-Mar-1999 #seqno=1, position 31 Mar-1999 #seqno=change 31-Dec-1999
 C:Accession: A23475
 R:Pratt, A.; Kallista, M.; Caron, F.; Meyer, E.
 J. Mol. Biol. 189, 47-60, 1985
 A:Title: Nucleotide sequence of the Parametium primurella G surface protein. A huge pro
 A:Reference number: A23475, MID:8704934
 A:Accession: A23475
 A:Molecule type: DNA
 A:Residues: 1-2718 <PRX>
 A:Note: The authors translated the codon TGC for residue 2665 as Trp
 C:Genetics:
 A:Genetic code: SGCS
 C:Superfamily: G surface protein

Query Match: 100.0%, Score 26, DB 2, Length 2718,
 Best Local Similarity: 100.0%, Prod No. 58002,
 Matches 5, Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 1 STISC 5
 Db 1487 STISC 1491

RESULT 8
 S10220
 sodium/proline symporter - Salmonella typhimurium
 A:Cross-references: 158 MISC01, NID:947850, PID:9407166
 C:Genetics:
 A:Gene: gfp-MIP
 A:Map position: 4331-4491
 A:Map position: 4331-4491
 C:Superfamily: unassigned eta-related proteins; eta transforming protein homology
 C:Keywords: DNA binding, transcription regulation, zinc finger
 F:661-680/Domain: eta transforming protein homology <EMBL>
 F:681-721/Domain: eta finger
 F:722-964/Domain: zinc finger

Query Match: 100.0%, Score 26, DB 2, Length 2718,
 Best Local Similarity: 100.0%, Prod No. 58002,
 Matches 5, Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 1 STISC 5
 Db 1487 STISC 1491

RESULT 9
 J02382
 sodium/proline symporter - Pseudomonas fluorescens
 N:Alternate names: proline permease
 C:Species: Pseudomonas fluorescens
 C:Date: 20-Feb-1999 #seqno=1, position 12 Feb-1999 #seqno=change 13-Sep-1999
 C:Accession: J02382
 R:Hosoya, H.; Nakamura, K.
 Biosci. Biotechnol. Biochem. 73, 2229-2301, 1994
 A:Title: DNA sequence of proline permease gene from Pseudomonas and predicted structure
 A:Reference number: J02382
 A:Accession: J02382
 A:Molecule type: DNA
 A:Residues: 1-494 <HOS>
 C:Function:
 A:Superfamily: eta-related proteins; eta transforming protein homology
 C:Keywords: proline transport, sodium transport, symport system, transmembrane protein
 F:2-56/Domain: transmembrane #status predicted <TM>
 F:46-73/Domain: transmembrane #status predicted <TM>
 F:128-147/Domain: transmembrane #status predicted <TM>
 F:163-185/Domain: transmembrane #status predicted <TM>
 F:191-210/Domain: transmembrane #status predicted <TM>
 F:211-230/Domain: transmembrane #status predicted <TM>
 F:231-250/Domain: transmembrane #status predicted <TM>
 F:251-271/Domain: transmembrane #status predicted <TM>
 F:272-291/Domain: transmembrane #status predicted <TM>
 F:292-311/Domain: transmembrane #status predicted <TM>
 F:312-331/Domain: transmembrane #status predicted <TM>
 F:332-351/Domain: transmembrane #status predicted <TM>
 F:352-371/Domain: transmembrane #status predicted <TM>
 F:372-391/Domain: transmembrane #status predicted <TM>
 F:392-411/Domain: transmembrane #status predicted <TM>
 F:412-431/Domain: transmembrane #status predicted <TM>
 F:432-451/Domain: transmembrane #status predicted <TM>
 F:452-471/Domain: transmembrane #status predicted <TM>
 F:472-491/Domain: transmembrane #status predicted <TM>

A:Molecule type: DNA
 A:Residues: 1-494 <HOS>
 R:Hosoya, H.; Nakamura, K.
 Biosci. Biotechnol. Biochem. 73, 2229-2301, 1994
 A:Title: DNA sequence of proline permease gene from Pseudomonas and predicted structure
 A:Reference number: J02382
 A:Accession: J02382
 A:Molecule type: DNA
 A:Residues: 1-494 <HOS>
 C:Function:
 A:Superfamily: eta-related proteins; eta transforming protein homology
 C:Keywords: proline transport, sodium transport, symport system, transmembrane protein
 F:2-56/Domain: transmembrane #status predicted <TM>
 F:46-73/Domain: transmembrane #status predicted <TM>
 F:128-147/Domain: transmembrane #status predicted <TM>
 F:163-185/Domain: transmembrane #status predicted <TM>
 F:191-210/Domain: transmembrane #status predicted <TM>
 F:211-230/Domain: transmembrane #status predicted <TM>
 F:231-250/Domain: transmembrane #status predicted <TM>
 F:251-271/Domain: transmembrane #status predicted <TM>
 F:272-291/Domain: transmembrane #status predicted <TM>
 F:292-311/Domain: transmembrane #status predicted <TM>
 F:312-331/Domain: transmembrane #status predicted <TM>
 F:332-351/Domain: transmembrane #status predicted <TM>
 F:352-371/Domain: transmembrane #status predicted <TM>
 F:372-391/Domain: transmembrane #status predicted <TM>
 F:392-411/Domain: transmembrane #status predicted <TM>
 F:412-431/Domain: transmembrane #status predicted <TM>
 F:432-451/Domain: transmembrane #status predicted <TM>
 F:452-471/Domain: transmembrane #status predicted <TM>
 F:472-491/Domain: transmembrane #status predicted <TM>

Query Match: 100.0%, Score 26, DB 2, Length 502,
 Best Local Similarity: 100.0%, Prod No. 15002,
 Matches 5, Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 1 STISC 5
 Db 340 STISC 344

RESULT 9
 J02382
 sodium/proline symporter - Pseudomonas fluorescens
 N:Alternate names: proline permease
 C:Species: Pseudomonas fluorescens
 C:Date: 20-Feb-1999 #seqno=1, position 12 Feb-1999 #seqno=change 13-Sep-1999
 C:Accession: J02382
 R:Hosoya, H.; Nakamura, K.
 Biosci. Biotechnol. Biochem. 73, 2229-2301, 1994
 A:Title: DNA sequence of proline permease gene from Pseudomonas and predicted structure
 A:Reference number: J02382
 A:Accession: J02382
 A:Molecule type: DNA
 A:Residues: 1-494 <HOS>
 C:Function:
 A:Superfamily: eta-related proteins; eta transforming protein homology
 C:Keywords: proline transport, sodium transport, symport system, transmembrane protein
 F:2-56/Domain: transmembrane #status predicted <TM>
 F:46-73/Domain: transmembrane #status predicted <TM>
 F:128-147/Domain: transmembrane #status predicted <TM>
 F:163-185/Domain: transmembrane #status predicted <TM>
 F:191-210/Domain: transmembrane #status predicted <TM>
 F:211-230/Domain: transmembrane #status predicted <TM>
 F:231-250/Domain: transmembrane #status predicted <TM>
 F:251-271/Domain: transmembrane #status predicted <TM>
 F:272-291/Domain: transmembrane #status predicted <TM>
 F:292-311/Domain: transmembrane #status predicted <TM>
 F:312-331/Domain: transmembrane #status predicted <TM>
 F:332-351/Domain: transmembrane #status predicted <TM>
 F:352-371/Domain: transmembrane #status predicted <TM>
 F:372-391/Domain: transmembrane #status predicted <TM>
 F:392-411/Domain: transmembrane #status predicted <TM>
 F:412-431/Domain: transmembrane #status predicted <TM>
 F:432-451/Domain: transmembrane #status predicted <TM>
 F:452-471/Domain: transmembrane #status predicted <TM>
 F:472-491/Domain: transmembrane #status predicted <TM>

Query Match 100.0% Score 26 DB 2 Length 104
 Best Local Similarity 100.0% Prod No 140002
 Matches 5 Conservative 0 Mismatches 0 Indels 0 Gaps 0

1 STISC 5
 ||||
 DB 164 STISC 164

RESULT 1

1. Division control protein nkd1 (nkd1 yeast (Schizosaccharomyces pombe))
 C:Species: Schizosaccharomyces pombe
 C:Date: 27-Jun-1994 #sequence revision 27-Jun-1994 #text_change 04-Sep-1999
 C:Accession: A46152
 C:Keywords: G protein-coupled receptor; status predicted <TM>
 F:129-159/Domain: transmembrane #status predicted <TM>
 F:180-203/Domain: transmembrane #status predicted <TM>
 F:234-257/Domain: transmembrane #status predicted <TM>
 F:264-286/Domain: transmembrane #status predicted <TM>
 F:415-421/Binding site: calcium (Asn) (covalent) #status predicted
 F:302/Binding site: palmitate (Cys) (covalent) #status predicted
 A:Accession: A46152
 A:Status: preliminary not compared with conceptual translation
 A:Note: G protein-coupled receptor
 A:Keywords: cell division control; DNA binding; nucleus; transcription regulation
 F:129-159/Domain: transmembrane #status predicted <TM>

Query Match 100.0% Score 26 DB 2 Length 720
 Best Local Similarity 100.0% Prod No 20002
 Matches 5 Conservative 0 Mismatches 0 Indels 0 Gaps 0

1 STISC 5
 ||||
 DB 164 STISC 164

RESULT 1

1. Division control protein nkd1 (nkd1 yeast (Schizosaccharomyces pombe))
 C:Species: Schizosaccharomyces pombe
 C:Date: 27-Jun-1994 #sequence revision 27-Jun-1994 #text_change 13-Sep-1999
 C:Accession: A46152
 C:Keywords: G protein-coupled receptor; status predicted <TM>
 F:129-159/Domain: transmembrane #status predicted <TM>
 F:180-203/Domain: transmembrane #status predicted <TM>
 F:234-257/Domain: transmembrane #status predicted <TM>
 F:264-286/Domain: transmembrane #status predicted <TM>
 F:415-421/Binding site: calcium (Asn) (covalent) #status predicted
 F:302/Binding site: palmitate (Cys) (covalent) #status predicted
 A:Accession: A46152
 A:Status: preliminary not compared with conceptual translation
 A:Note: G protein-coupled receptor
 A:Keywords: cell division control; DNA binding; nucleus; transcription regulation
 F:129-159/Domain: transmembrane #status predicted <TM>

Query Match 100.0% Score 26 DB 2 Length 337
 Best Local Similarity 100.0% Prod No 110002
 Matches 5 Conservative 0 Mismatches 0 Indels 0 Gaps 0

1 STISC 5
 ||||
 DB 164 STISC 164

RESULT 1

1. Division control protein nkd1 (nkd1 yeast (Schizosaccharomyces pombe))
 C:Species: Schizosaccharomyces pombe
 C:Date: 27-Jun-1994 #sequence revision 27-Jun-1994 #text_change 13-Sep-1999
 C:Accession: A46152
 A:Status: preliminary not compared with conceptual translation
 A:Note: G protein-coupled receptor
 A:Keywords: cell division control; DNA binding; nucleus; transcription regulation
 F:129-159/Domain: transmembrane #status predicted <TM>

1. Division control protein nkd1 (nkd1 yeast (Schizosaccharomyces pombe))
 C:Species: Schizosaccharomyces pombe
 C:Date: 27-Jun-1994 #sequence revision 27-Jun-1994 #text_change 13-Sep-1999
 C:Accession: A46152
 A:Status: preliminary not compared with conceptual translation
 A:Note: G protein-coupled receptor
 A:Keywords: cell division control; DNA binding; nucleus; transcription regulation
 F:129-159/Domain: transmembrane #status predicted <TM>

Query Match 100.0% Score 26 DB 2 Length 320
 Best Local Similarity 100.0% Prod No 10002
 Matches 5 Conservative 0 Mismatches 0 Indels 0 Gaps 0

1 STISC 5
 ||||
 DB 164 STISC 168

RESULT 13
 A46152
 A3: adenosine receptor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 21-Sep-1993 #sequence revision 19-Nov-1994 #text_change 13-Sep-1999
 C:Accession: A46152
 R: Zhou, Q.Y.; Li, G.; Olab, M.E.; Johnson, R.A.; Still, G.M.; Civelli, V.
 Proc. Natl. Acad. Sci. U.S.A. 89, 7432-7436, 1992
 A:Title: Molecular cloning and characterization of an adenosine receptor (A46152)
 A:Reference number: A46152; MIM:193364475
 A:Accession: A46152
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-172 (CHO)
 A:Cross-references: MIM:193364475
 A:Experimental source: brain
 A:Note: sequence inconsistent with the nucleotide translation
 A:Note: sequence extracted from NRI backbone (MIM:110666) NRI:110666
 C:Superfamily: adenosine receptor A1
 C:Keywords: G protein coupled receptor; transmembrane protein

Query Match 100.0% Score 26 DB 2 Length 320
 Best Local Similarity 100.0% Prod No 10002
 Matches 5 Conservative 0 Mismatches 0 Indels 0 Gaps 0

1 STISC 5
 ||||
 DB 164 STISC 168

RESULT 14
 H64148
 hypothetical protein H64148 Haemophilus influenzae (strain H3N2)
 C:Species: Haemophilus influenzae
 C:Date: 18-Aug-1995 #sequence revision 18-Aug-1995 #text_change 30-Jun-1998
 C:Accession: H64148
 R: Fleischman, R.D.; Adams, M.D.; White, O.; Clayton, P.A.; Kroll, E.B.; Fink, J.
 Science 269, 496-512, 1995
 A:Authors: Fleischman, R.D.; Adams, M.D.; White, O.; Clayton, P.A.; Kroll, E.B.; Fink, J.
 Virology 199, 1-10, 1995
 A:Title: Whole genome random sequencing and assembly of Haemophilus influenzae Rd.

Query Match 100.0% Score 26 DB 2 Length 320
 Best Local Similarity 100.0% Prod No 10002
 Matches 5 Conservative 0 Mismatches 0 Indels 0 Gaps 0

1 STISC 5
 ||||
 DB 164 STISC 168

RESULT 14
 H64148
 hypothetical protein H64148 Haemophilus influenzae (strain H3N2)
 C:Species: Haemophilus influenzae
 C:Date: 18-Aug-1995 #sequence revision 18-Aug-1995 #text_change 30-Jun-1998
 C:Accession: H64148
 R: Fleischman, R.D.; Adams, M.D.; White, O.; Clayton, P.A.; Kroll, E.B.; Fink, J.
 Science 269, 496-512, 1995
 A:Authors: Fleischman, R.D.; Adams, M.D.; White, O.; Clayton, P.A.; Kroll, E.B.; Fink, J.
 Virology 199, 1-10, 1995
 A:Title: Whole genome random sequencing and assembly of Haemophilus influenzae Rd.

Query Match 100.0% Score 26 DB 2 Length 320
 Best Local Similarity 100.0% Prod No 10002
 Matches 5 Conservative 0 Mismatches 0 Indels 0 Gaps 0

1 STISC 5
 ||||
 DB 164 STISC 168

RESULT 14
 H64148
 hypothetical protein H64148 Haemophilus influenzae (strain H3N2)
 C:Species: Haemophilus influenzae
 C:Date: 18-Aug-1995 #sequence revision 18-Aug-1995 #text_change 30-Jun-1998
 C:Accession: H64148
 R: Fleischman, R.D.; Adams, M.D.; White, O.; Clayton, P.A.; Kroll, E.B.; Fink, J.
 Science 269, 496-512, 1995
 A:Authors: Fleischman, R.D.; Adams, M.D.; White, O.; Clayton, P.A.; Kroll, E.B.; Fink, J.
 Virology 199, 1-10, 1995
 A:Title: Whole genome random sequencing and assembly of Haemophilus influenzae Rd.

Query Match 100.0% Score 26 DB 2 Length 320
 Best Local Similarity 100.0% Prod No 10002
 Matches 5 Conservative 0 Mismatches 0 Indels 0 Gaps 0

1 STISC 5
 ||||
 DB 164 STISC 168

RESULT 14
 H64148
 hypothetical protein H64148 Haemophilus influenzae (strain H3N2)
 C:Species: Haemophilus influenzae
 C:Date: 18-Aug-1995 #sequence revision 18-Aug-1995 #text_change 30-Jun-1998
 C:Accession: H64148
 R: Fleischman, R.D.; Adams, M.D.; White, O.; Clayton, P.A.; Kroll, E.B.; Fink, J.
 Science 269, 496-512, 1995
 A:Authors: Fleischman, R.D.; Adams, M.D.; White, O.; Clayton, P.A.; Kroll, E.B.; Fink, J.
 Virology 199, 1-10, 1995
 A:Title: Whole genome random sequencing and assembly of Haemophilus influenzae Rd.

A:Reference number: A64000; MIP:4545030

A:Accession: H64148

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1113 (1988)

A:Note: best homolog was a hypothetical protein from Escherichia coli

Query Match

Best Local Similarity: 100.0%; Score 26; DB 2; Length 113;

Matches: 5; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

OY 1 STISC 5

DB 17 STISC 21

Result 15

E71484

C:Probable GMP kinase - Chlamydia trachomatis (serotype D, strain UW3/Cx)

C:Species: Chlamydia trachomatis

C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 13-Sep-1998

C:Accession: E71484

P:Stephens, R.S.; Kaitan, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, submitted to Genbank, May 1998

A:Description: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia

A:Reference number: A71460

A:Accession: E71484

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-245 (ARNP)

A:Cross-reference: GP:AE001728, GP:AE001773, NID:J3322126, PID:G3322130

A:Experimental source: serotype D, strain UW-3/Cx

C:Genetics:

A:Gene: pyrH

Query Match

Best Local Similarity: 100.0%; Score 26; DB 2; Length 245;

Matches: 5; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

OY 1 STISC 5

DB 105 STISC 109

Search completed: June 22, 1999, 10:58:50
Job time: 149 sec



Query Match Score 26 DB 1 Length 759
Best local similarity 100.0% Prod. No. 4.6e-02
Matches 5 Conservative 0 Mismatches 0 Indels 0 Gaps 0

Sequence 509 AA:
PT peptide from sperm surface protein which stimulates antibody
PT proin.
PS Example 4; Fig 4; 79pp: English.
CC Sperm surface proteins or peptides stimulate an immune response to
CC produce antibodies which block sperm-egg fusion and provide
CC contraception. Pref. sperm surface proteins are the PH-20 and PH-30
CC sperm surface proteins.
SQ Sequence 509 AA:

DB 439 STISC 443

RESULT 5

AC R47349 standard; protein; 275 AA.

DE Human PH-20 (first entry)

DE Human PH-20 (derived from partial clone H16).

DE Sperm surface protein which stimulates antibody response.

DE Homo sapiens.

DE Homo sapiens.

DE Homo sapiens.

DE Homo sapiens.

DE Homo sapiens.

DE Homo sapiens.

DE Homo sapiens.

DE Homo sapiens.

DE Homo sapiens.

DE Homo sapiens.

DE Homo sapiens.

DE Homo sapiens.

DE Homo sapiens.

DE Homo sapiens.

DE Homo sapiens.

DE Homo sapiens.

DE Homo sapiens.

DE Homo sapiens.

DE Homo sapiens.

DE Homo sapiens.

DE Homo sapiens.

DE Homo sapiens.

DE Homo sapiens.

DE Homo sapiens.

DE Homo sapiens.

DE Homo sapiens.

DE Homo sapiens.

Query Match Score 26 DB 1 Length 275
Best local similarity 100.0% Prod. No. 2.6e-02
Matches 5 Conservative 0 Mismatches 0 Indels 0 Gaps 0

Sequence 275 AA:
PT peptide from sperm surface protein which stimulates antibody
PT proin.
PS Example 4; Fig 4; 79pp: English.
CC Sperm surface proteins or peptides stimulate an immune response to
CC produce antibodies which block sperm-egg fusion and provide
CC contraception. Pref. sperm surface proteins are the PH-20 and PH-30
CC sperm surface proteins.
SQ Sequence 275 AA:

DB 204 STISC 208

UY 1 STISC 5

DB 204 STISC 208

UY 1 STISC 5

DB 204 STISC 208

UY 1 STISC 5

Query Match Score 26 DB 1 Length 275
Best local similarity 100.0% Prod. No. 2.6e-02
Matches 5 Conservative 0 Mismatches 0 Indels 0 Gaps 0

Sequence 275 AA:
PT peptide from sperm surface protein which stimulates antibody
PT proin.
PS Example 4; Fig 4; 79pp: English.
CC Sperm surface proteins or peptides stimulate an immune response to
CC produce antibodies which block sperm-egg fusion and provide
CC contraception. Pref. sperm surface proteins are the PH-20 and PH-30
CC sperm surface proteins.
SQ Sequence 275 AA:

UY 1 STISC 5

DB 204 STISC 208

UY 1 STISC 5

DB 204 STISC 208

UY 1 STISC 5

DB 204 STISC 208

Query Match Score 26 DB 1 Length 275
Best local similarity 100.0% Prod. No. 2.6e-02
Matches 5 Conservative 0 Mismatches 0 Indels 0 Gaps 0

Sequence 275 AA:
PT peptide from sperm surface protein which stimulates antibody
PT proin.
PS Example 4; Fig 4; 79pp: English.
CC Sperm surface proteins or peptides stimulate an immune response to
CC produce antibodies which block sperm-egg fusion and provide
CC contraception. Pref. sperm surface proteins are the PH-20 and PH-30
CC sperm surface proteins.
SQ Sequence 275 AA:

UY 1 STISC 5

DB 204 STISC 208

UY 1 STISC 5

DB 204 STISC 208

UY 1 STISC 5

DB 204 STISC 208

CC Expression of activity. The protein can also be used to diagnose, prevent
 CC or treat IDIF-2 induction of proliferation, differentiation or maturation
 CC of leukocytes at lymphocytes, especially in relation to tissue damage
 CC associated with inflammation
 CC Sequence 193 AA:

Query Match 100.0% Score 26; DB 1; Length 193;
 Best Local Similarity 100.0% Pred No 1 4e-02;

Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STISC 5
 DB 108 STISC 112

RESULT 13
 W15704
 ID W15704 standard; peptide: 193 AA

AC W15704
 DI 26 JAN-1998 (first entry)

DE Mouse interferon-gamma inducer protein.

KM Interferon-gamma, IFN-gamma; antiviral; antitoxic; radiotherapy;
 KW immunoregulatory; antitumor agent; chemotherapy; leukopenia;
 KW chemocytotoxic; immunocompetent cell; asthma; hayfever;
 KW rheumatism; interleukin-1 killer cell

OS Mus musculus.

FT Key Location/Qualifiers

FI Misc-differences 70

PN EP-76779-A1; (label) Met; Thr

PD 09-APR-1997; 206597

FE 26-SEP-1997; 206597

FR 20-SEP-1997; 206597

PR 26-SEP-1997; 206597

PA 26-SEP-1997; 206597

PI 26-SEP-1997; 206597

DR N-PSDB: 160536

FI Human protein that induces interferon-gamma prodn. in

FI immunocompetent cells. Useful for adoptive immunotherapy of

FI tumours and as antimicrobial agent etc.

PS Discussed: Page 22; 26pp; English.

CC The present sequence represents a novel protein from mouse liver cells,

CC which induces interferon-gamma (IFN gamma) production in immunocompetent

CC cells. This protein enhances cytotoxicity of killer cells and induces

CC their formation. It is used as an antitoxic agent for antitumor

CC immunotherapy, an antiviral (including anti-AIDS) or antibacterial agent,

CC and in the treatment of atopic or immune system diseases, e.g. asthma,

CC hayfever or rheumatism. When formulated with interleukin-3, it is also

CC used to treat leukemia and thrombocytopenia associated with

CC radiation or chemotherapy of leukemia and other cancers. When used

CC in antitumor immunotherapy, this novel protein significantly improves

CC the immunotherapeutic effect of interleukin-2 (IL-2). (prepared with use

CC of IL-2 alone, either when administered to the patient (before

CC administration of IL-2) or by addition to the medium in which cells

CC (dispensed for return to the patient) are being grown

CC Sequence 193 AA:

AC W15704
 DI 01-APR-1998 (first entry)
 DE Peptide sequence #4 displayed by RSW17 minotope phages.
 KW Peptide immunogen; vaccination; allergy; epidermis; immune response
 KW immunoglobulin E; antibody RSW17; atopic dermatitis; RSW17; RSW17
 KW antibody; mast cell; basophil; immunisation; minotope phage; circular
 OS Synthetic.

OS Homo sapiens.

FT Key Location/Qualifiers

FI Key 100.0% Score 26; DB 1; Length 9;
 Best Local Similarity 100.0% Pred No 1 3e-05;

Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STISC 5
 DB 5 STISC 9

RESULT 15
 W46592
 ID W46592 standard; protein: 193 AA.

AC W46592
 DI 21-MAY-1998 (first entry)

DE Amino acid sequence of human interleukin-1-gamma.

KW Interleukin-1-gamma, IL-1-gamma; mouse; cytokine; IDIF; interferon-gamma;
 KW biological activity; biological assay; protein; protein activity;
 OS Homo sapiens.

FT Key Location/Qualifiers

FI Key 100.0% Score 26; DB 1; Length 9;
 Best Local Similarity 100.0% Pred No 1 3e-05;

Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STISC 5
 DB 5 STISC 9

RESULT 15
 W46592
 ID W46592 standard; protein: 193 AA.

AC W46592
 DI 21-MAY-1998 (first entry)

DE Amino acid sequence of human interleukin-1-gamma.

KW Interleukin-1-gamma, IL-1-gamma; mouse; cytokine; IDIF; interferon-gamma;
 KW biological activity; biological assay; protein; protein activity;
 OS Homo sapiens.

FT Key Location/Qualifiers

FI Key 100.0% Score 26; DB 1; Length 9;
 Best Local Similarity 100.0% Pred No 1 3e-05;

Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STISC 5
 DB 5 STISC 9

RESULT 15
 W46592
 ID W46592 standard; protein: 193 AA.

AC W46592
 DI 21-MAY-1998 (first entry)

DE Amino acid sequence of human interleukin-1-gamma.

KW Interleukin-1-gamma, IL-1-gamma; mouse; cytokine; IDIF; interferon-gamma;
 KW biological activity; biological assay; protein; protein activity;
 OS Homo sapiens.

FT Key Location/Qualifiers

FI Key 100.0% Score 26; DB 1; Length 9;
 Best Local Similarity 100.0% Pred No 1 3e-05;

Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Genome version 4.5
Copyright (c) 1999 - 1998 Cofwper Ltd

OM protein - protein search, using sw model

Run on: June 23, 1999 11:01:22 : Search time 23.17 Seconds

(without alignments)

3,317 Million cell updates/sec

Title: US-09-030-061-5

Perfect score: 26

Sequence: 1 stlcr 5

Scoring table: BLOSUM62

Searched: 180763 seqs, 55169189 residues

Database:

SPRMBL_8:
1: sp.fungi:
2: sp.human:
3: sp.invertebrate:
4: sp.mammal:
5: sp.pho:
6: sp.oxanole:
7: sp.phage:
8: sp.plant:
9: sp.bacteria:
10: sp.fungi:
11: sp.virus:
12: sp.yeast:
13: sp.unclassified:
14: sp.archaea:

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	100.0	994	1	007454 saccharomy
2	26	100.0	489	2	013787 homo sapien
3	26	100.0	193	2	005509
4	26	100.0	747	3	009586 caenorhabd
5	26	100.0	233	3	009586 caenorhabd
6	26	100.0	332	3	016644 caenorhabd
7	26	100.0	446	3	018276 caenorhabd
8	26	100.0	489	9	047551 escherichia
9	26	100.0	489	9	047552 escherichia
10	26	100.0	489	9	047552 escherichia
11	26	100.0	489	9	047552 escherichia
12	26	100.0	489	9	047552 escherichia
13	26	100.0	489	9	047552 escherichia
14	26	100.0	489	9	047552 escherichia
15	26	100.0	489	9	047552 escherichia
16	26	100.0	489	9	047552 escherichia
17	26	100.0	489	9	047552 escherichia
18	26	100.0	489	9	047552 escherichia
19	26	100.0	489	9	047552 escherichia
20	26	100.0	489	9	047552 escherichia
21	26	100.0	489	9	047552 escherichia
22	26	100.0	489	9	047552 escherichia
23	26	100.0	489	9	047552 escherichia
24	26	100.0	489	9	047552 escherichia
25	26	100.0	489	9	047552 escherichia
26	26	100.0	489	9	047552 escherichia
27	26	100.0	489	9	047552 escherichia
28	26	100.0	489	9	047552 escherichia
29	26	100.0	489	9	047552 escherichia
30	26	100.0	489	9	047552 escherichia

ALIGNMENTS

Result	ID	Query Match	Score	DB ID	Length	Prod. No.	Matches	Mismatches	Gaps
1	007454	PRELIMINARY	984	AA					
2	013787	PRELIMINARY	4560	AA					
3	013787	PRELIMINARY	4560	AA					
4	013787	PRELIMINARY	4560	AA					
5	013787	PRELIMINARY	4560	AA					
6	013787	PRELIMINARY	4560	AA					
7	013787	PRELIMINARY	4560	AA					
8	013787	PRELIMINARY	4560	AA					
9	013787	PRELIMINARY	4560	AA					
10	013787	PRELIMINARY	4560	AA					
11	013787	PRELIMINARY	4560	AA					
12	013787	PRELIMINARY	4560	AA					
13	013787	PRELIMINARY	4560	AA					
14	013787	PRELIMINARY	4560	AA					
15	013787	PRELIMINARY	4560	AA					
16	013787	PRELIMINARY	4560	AA					
17	013787	PRELIMINARY	4560	AA					
18	013787	PRELIMINARY	4560	AA					
19	013787	PRELIMINARY	4560	AA					
20	013787	PRELIMINARY	4560	AA					
21	013787	PRELIMINARY	4560	AA					
22	013787	PRELIMINARY	4560	AA					
23	013787	PRELIMINARY	4560	AA					
24	013787	PRELIMINARY	4560	AA					
25	013787	PRELIMINARY	4560	AA					
26	013787	PRELIMINARY	4560	AA					
27	013787	PRELIMINARY	4560	AA					
28	013787	PRELIMINARY	4560	AA					
29	013787	PRELIMINARY	4560	AA					
30	013787	PRELIMINARY	4560	AA					

25 STING 11
 26 STING 11
 27 STING 11
 28 STING 11
 29 STING 11
 30 STING 11
 31 STING 11
 32 STING 11
 33 STING 11
 34 STING 11
 35 STING 11
 36 STING 11
 37 STING 11
 38 STING 11
 39 STING 11
 40 STING 11
 41 STING 11
 42 STING 11
 43 STING 11
 44 STING 11
 45 STING 11
 46 STING 11
 47 STING 11
 48 STING 11
 49 STING 11
 50 STING 11
 51 STING 11
 52 STING 11
 53 STING 11
 54 STING 11
 55 STING 11
 56 STING 11
 57 STING 11
 58 STING 11
 59 STING 11
 60 STING 11
 61 STING 11
 62 STING 11
 63 STING 11
 64 STING 11
 65 STING 11
 66 STING 11
 67 STING 11
 68 STING 11
 69 STING 11
 70 STING 11
 71 STING 11
 72 STING 11
 73 STING 11
 74 STING 11
 75 STING 11
 76 STING 11
 77 STING 11
 78 STING 11
 79 STING 11
 80 STING 11
 81 STING 11
 82 STING 11
 83 STING 11
 84 STING 11
 85 STING 11
 86 STING 11
 87 STING 11
 88 STING 11
 89 STING 11
 90 STING 11
 91 STING 11
 92 STING 11
 93 STING 11
 94 STING 11
 95 STING 11
 96 STING 11
 97 STING 11
 98 STING 11
 99 STING 11
 100 STING 11

101 STING 11
 102 STING 11
 103 STING 11
 104 STING 11
 105 STING 11
 106 STING 11
 107 STING 11
 108 STING 11
 109 STING 11
 110 STING 11
 111 STING 11
 112 STING 11
 113 STING 11
 114 STING 11
 115 STING 11
 116 STING 11
 117 STING 11
 118 STING 11
 119 STING 11
 120 STING 11
 121 STING 11
 122 STING 11
 123 STING 11
 124 STING 11
 125 STING 11
 126 STING 11
 127 STING 11
 128 STING 11
 129 STING 11
 130 STING 11
 131 STING 11
 132 STING 11
 133 STING 11
 134 STING 11
 135 STING 11
 136 STING 11
 137 STING 11
 138 STING 11
 139 STING 11
 140 STING 11
 141 STING 11
 142 STING 11
 143 STING 11
 144 STING 11
 145 STING 11
 146 STING 11
 147 STING 11
 148 STING 11
 149 STING 11
 150 STING 11
 151 STING 11
 152 STING 11
 153 STING 11
 154 STING 11
 155 STING 11
 156 STING 11
 157 STING 11
 158 STING 11
 159 STING 11
 160 STING 11
 161 STING 11
 162 STING 11
 163 STING 11
 164 STING 11
 165 STING 11
 166 STING 11
 167 STING 11
 168 STING 11
 169 STING 11
 170 STING 11
 171 STING 11
 172 STING 11
 173 STING 11
 174 STING 11
 175 STING 11
 176 STING 11
 177 STING 11
 178 STING 11
 179 STING 11
 180 STING 11
 181 STING 11
 182 STING 11
 183 STING 11
 184 STING 11
 185 STING 11
 186 STING 11
 187 STING 11
 188 STING 11
 189 STING 11
 190 STING 11
 191 STING 11
 192 STING 11
 193 STING 11
 194 STING 11
 195 STING 11
 196 STING 11
 197 STING 11
 198 STING 11
 199 STING 11
 200 STING 11

CC: 1. SUBMITTER: EPYQNS TO THE LIGAND-GATED IONIC CHANNELS FAMILY
DR EMBL: 263267, F1186516; -
LE PROSITE: PS00336; NEUROTRP_ION_CHANNEL.1.

RT	Salmonella and Escherichia coll.":
PL	J. BACTERIOL. 174:886-896 (1992).
LN	EMBL, L01452. 9147443.

PF SITE 150477 NA_SOUT_SYP_2; 1.
 ID 054978 PRELIMINARY; PRT: 489 AA.
 AC 054978; PRT: 489 AA.
 DR PROSITE: PS00457; NA_SOUT_SYP_2; 1.
 FT NON_TER 489 489
 SO SEQUENCE 489 AA; 52901 MW; 701197RR CRC32;

Query Match 100.0%; Score 26; DB 9; Length 489;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 STISC 5
 Db 340 STISC 344

RESULT 12
 ID 054978 PRELIMINARY; PRT: 489 AA.
 AC 054978; PRT: 489 AA.
 DR PROSITE: PS00457; NA_SOUT_SYP_2; 1.
 FT NON_TER 489 489
 SO SEQUENCE 489 AA; 52901 MW; 701197RR CRC32;

01 NOV-1996 (TREMBLER, 01, CREATED)
 02 NOV-1996 (TREMBLER, 01, LAST SEQUENCE UPDATE)
 03 NOV-1996 (TREMBLER, 08, LAST ANNOTATION UPDATE)
 04 PROLINE PERMEASE (FRAGMENT).
 05 BACTERIA: GAMMA SUBDIVISION: ENTEROBACTERIACEAE;
 06 BACTERIA: PROTEOBACTERIA: GAMMA SUBDIVISION: ENTEROBACTERIACEAE;
 07 ESCHERICHIA COLI.
 08 BACTERIA: PROTEOBACTERIA: GAMMA SUBDIVISION: ENTEROBACTERIACEAE;
 09 ESCHERICHIA COLI.
 10 SEQUENCE FROM N.A.
 11 NELSON K., SELANDER R.K.;
 12 "Evolutionary genetics of the proline permease gene (putP) and the control region of the proline utilization operon in populations of *Salmonella* and *Escherichia coli*.";
 13 EMBL: L01136; G154292; - (895)(3932).
 14 PROSITE: PS00457; NA_SOUT_SYP_2; 1.
 15 PROSITE: PS00457; NA_SOUT_SYP_2; 1.
 16 PFW: PF00474; SSF: 1.
 17 NON_TER 489 489
 18 SEQUENCE 489 AA; 52901 MW; 19700000 CRC32;

Query Match 100.0%; Score 26; DB 9; Length 489;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 STISC 5
 Db 340 STISC 344

RESULT 13
 ID 054978 PRELIMINARY; PRT: 489 AA.
 AC 054978; PRT: 489 AA.
 DR PROSITE: PS00457; NA_SOUT_SYP_2; 1.
 FT NON_TER 489 489
 SO SEQUENCE 489 AA; 52901 MW; 701197RR CRC32;

01 NOV-1996 (TREMBLER, 01, CREATED)
 02 NOV-1996 (TREMBLER, 01, LAST SEQUENCE UPDATE)
 03 NOV-1996 (TREMBLER, 08, LAST ANNOTATION UPDATE)
 04 PROLINE PERMEASE (FRAGMENT).
 05 BACTERIA: GAMMA SUBDIVISION: ENTEROBACTERIACEAE;
 06 BACTERIA: PROTEOBACTERIA: GAMMA SUBDIVISION: ENTEROBACTERIACEAE;
 07 ESCHERICHIA COLI.
 08 BACTERIA: PROTEOBACTERIA: GAMMA SUBDIVISION: ENTEROBACTERIACEAE;
 09 ESCHERICHIA COLI.
 10 SEQUENCE FROM N.A.
 11 NELSON K., SELANDER R.K.;
 12 "Evolutionary genetics of the proline permease gene (putP) and the control region of the proline utilization operon in populations of *Salmonella* and *Escherichia coli*.";
 13 EMBL: L01136; G154292; - (895)(3932).
 14 PROSITE: PS00457; NA_SOUT_SYP_2; 1.
 15 PROSITE: PS00457; NA_SOUT_SYP_2; 1.
 16 PFW: PF00474; SSF: 1.
 17 NON_TER 489 489
 18 SEQUENCE 489 AA; 52901 MW; 19700000 CRC32;

DR PROSITE: PS00456; NA_SOUT_SYP_1; 1.
 DR PROSITE: PS00457; NA_SOUT_SYP_2; 1.
 DR PFW: PF00474; SSF: 1.
 FT NON_TER 489 489
 SO SEQUENCE 489 AA; 52901 MW; 701197RR CRC32;

Query Match 100.0%; Score 26; DB 9; Length 489;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 STISC 5
 Db 340 STISC 344

RESULT 12
 ID 054978 PRELIMINARY; PRT: 489 AA.
 AC 054978; PRT: 489 AA.
 DR PROSITE: PS00457; NA_SOUT_SYP_2; 1.
 FT NON_TER 489 489
 SO SEQUENCE 489 AA; 52901 MW; 701197RR CRC32;

01 NOV-1996 (TREMBLER, 01, CREATED)
 02 NOV-1996 (TREMBLER, 01, LAST SEQUENCE UPDATE)
 03 NOV-1996 (TREMBLER, 08, LAST ANNOTATION UPDATE)
 04 PROLINE PERMEASE (FRAGMENT).
 05 BACTERIA: GAMMA SUBDIVISION: ENTEROBACTERIACEAE;
 06 BACTERIA: PROTEOBACTERIA: GAMMA SUBDIVISION: ENTEROBACTERIACEAE;
 07 ESCHERICHIA COLI.
 08 BACTERIA: PROTEOBACTERIA: GAMMA SUBDIVISION: ENTEROBACTERIACEAE;
 09 ESCHERICHIA COLI.
 10 SEQUENCE FROM N.A.
 11 NELSON K., SELANDER R.K.;
 12 "Evolutionary genetics of the proline permease gene (putP) and the control region of the proline utilization operon in populations of *Salmonella* and *Escherichia coli*.";
 13 EMBL: L01136; G154292; - (895)(3932).
 14 PROSITE: PS00456; NA_SOUT_SYP_1; 1.
 15 PROSITE: PS00457; NA_SOUT_SYP_2; 1.
 16 PFW: PF00474; SSF: 1.
 17 NON_TER 489 489
 18 SEQUENCE 489 AA; 52901 MW; 19700000 CRC32;

Query Match 100.0%; Score 26; DB 9; Length 489;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 STISC 5
 Db 340 STISC 344

RESULT 13
 ID 054978 PRELIMINARY; PRT: 489 AA.
 AC 054978; PRT: 489 AA.
 DR PROSITE: PS00457; NA_SOUT_SYP_2; 1.
 FT NON_TER 489 489
 SO SEQUENCE 489 AA; 52901 MW; 701197RR CRC32;

01 NOV-1996 (TREMBLER, 01, CREATED)
 02 NOV-1996 (TREMBLER, 01, LAST SEQUENCE UPDATE)
 03 NOV-1996 (TREMBLER, 08, LAST ANNOTATION UPDATE)
 04 PROLINE PERMEASE (FRAGMENT).
 05 BACTERIA: GAMMA SUBDIVISION: ENTEROBACTERIACEAE;
 06 BACTERIA: PROTEOBACTERIA: GAMMA SUBDIVISION: ENTEROBACTERIACEAE;
 07 ESCHERICHIA COLI.
 08 BACTERIA: PROTEOBACTERIA: GAMMA SUBDIVISION: ENTEROBACTERIACEAE;
 09 ESCHERICHIA COLI.
 10 SEQUENCE FROM N.A.
 11 NELSON K., SELANDER R.K.;
 12 "Evolutionary genetics of the proline permease gene (putP) and the control region of the proline utilization operon in populations of *Salmonella* and *Escherichia coli*.";
 13 EMBL: L01136; G154292; - (895)(3932).
 14 PROSITE: PS00457; NA_SOUT_SYP_2; 1.
 15 PROSITE: PS00457; NA_SOUT_SYP_2; 1.
 16 PFW: PF00474; SSF: 1.
 17 NON_TER 489 489
 18 SEQUENCE 489 AA; 52901 MW; 19700000 CRC32;

RL J. BACTERIOID 174:6886-6895(1992).
 DR EMBL: L01139: G154294.
 DR PROSITE: P80456: NA_SQUT_SYMP_1: 1.
 DR PROSITE: P80457: NA_SQUT_SYMP_2: 1.
 DR PIRAM: PF00474: SSF: 1.
 FT NON_TER 489 AA: 12367 MM: 6A13E319 CP0320.
 SEQUENCE 489 AA: 12367 MM: 6A13E319 CP0320.

Query Match 100.0%; Score 26; DB 9; Length 489;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STSC 5
 |||||
 Db 340 STSC 344

RESULT 14
 054980
 ID 054980 PRELIMINARY: PRT: 489 AA.

AC 054980: PRELIMINARY: PRT: 489 AA.
 DI 01-NOV-1996 (TREMPEL 01, CREATED)
 DT 01-NOV-1996 (TREMPEL 01, LAST SEQUENCE UPDATE)
 DE 01-NOV-1996 (TREMPEL 08, LAST ANNOTATION UPDATE)
 DE PROLINE PERMEASE (FRAGMENT).
 GN PUTP.
 OS SALMONELLA SP.
 OC BACTERIA: PROTEOBACTERIA: GAMMA SUBDIVISION: ENTEROBACTERIACEAE;
 OC SALMONELLA.
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN-S2980;
 RX MEDLINE: 93015751.
 RA NELSON K., SELANDER R.K.;
 RI "Evolutionary genetics of the proline permease gene (putp) and the
 RI control region of the proline utilization operon in populations of
 RI Salmonella and Escherichia coli."
 RL J. BACTERIOLOGY 174:6886-6895(1992).
 DR EMBL: L01139: G154294.
 DR PROSITE: P80456: NA_SQUT_SYMP_1: 1.
 DR PROSITE: P80457: NA_SQUT_SYMP_2: 1.
 DR PIRAM: PF00474: SSF: 1.
 FT NON_TER 489 AA: 12367 MM: 6A13E319 CP0320.
 SEQUENCE 489 AA: 12367 MM: 6A13E319 CP0320.

Query Match 100.0%; Score 26; DB 9; Length 489;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STSC 5
 |||||
 Db 340 STSC 344

RESULT 15
 054981

ID 054981 PRELIMINARY: PRT: 489 AA

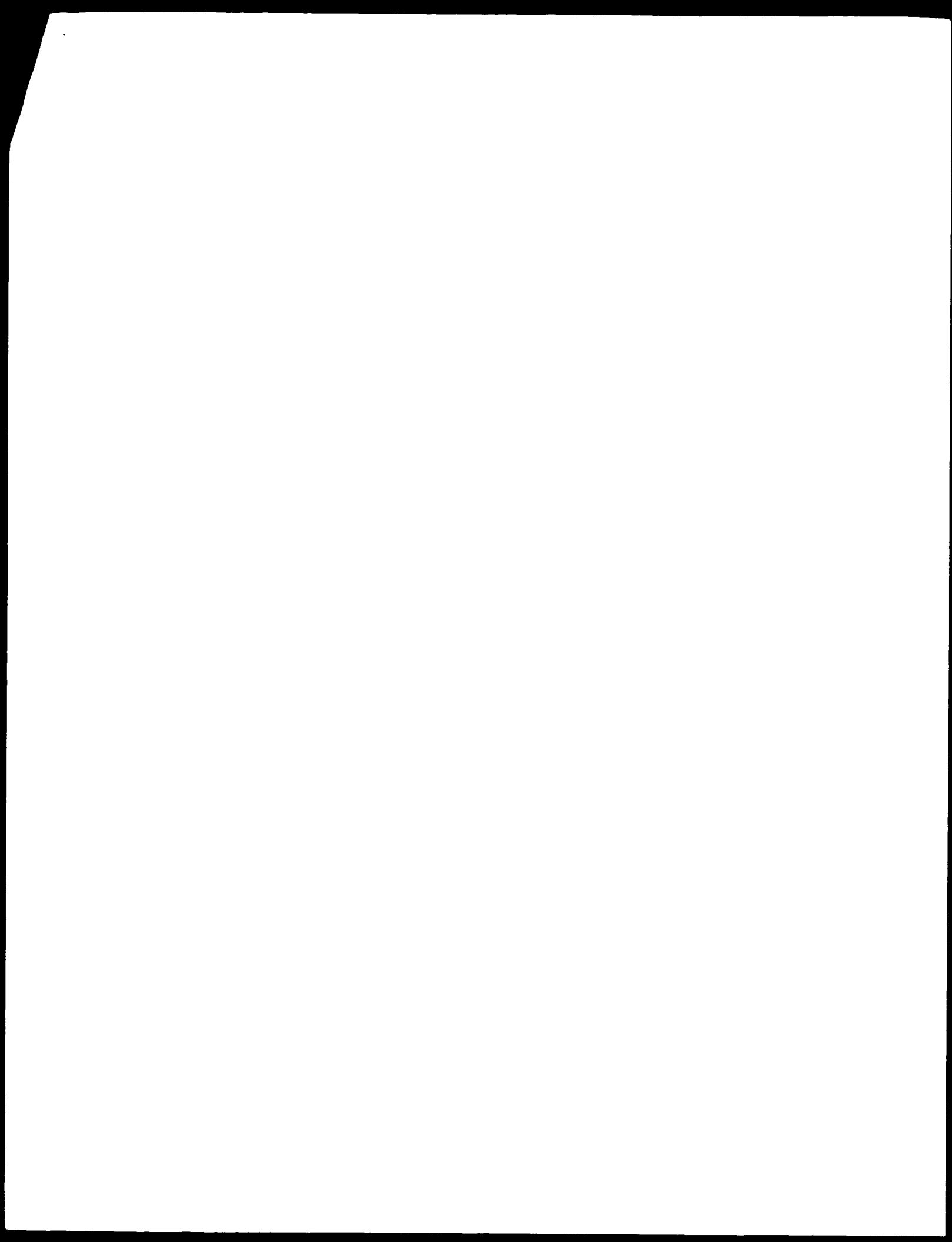
AC 054981: PRELIMINARY: PRT: 489 AA.
 DI 01-NOV-1996 (TREMPEL 01, CREATED)
 DT 01-NOV-1996 (TREMPEL 01, LAST SEQUENCE UPDATE)
 DE 01-NOV-1996 (TREMPEL 08, LAST ANNOTATION UPDATE)
 DE PROLINE PERMEASE (FRAGMENT).
 GN PUTP.
 OS SALMONELLA SP.
 OC BACTERIA: PROTEOBACTERIA: GAMMA SUBDIVISION: ENTEROBACTERIACEAE;
 OC SALMONELLA.
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN-S2980;
 RX MEDLINE: 93015751.
 RA NELSON K., SELANDER R.K.;

RI "Evolutionary genetics of the proline permease gene (putp) and the
 RI control region of the proline utilization operon in populations of
 RI Salmonella and Escherichia coli."
 RL J. BACTERIOLOGY 174:6886-6895(1992).
 DR EMBL: L01139: G154294.
 DR PROSITE: P80456: NA_SQUT_SYMP_1: 1.
 DR PROSITE: P80457: NA_SQUT_SYMP_2: 1.
 DR PIRAM: PF00474: SSF: 1.
 FT NON_TER 489 AA: 12367 MM: 6A13E319 CP0320.
 SEQUENCE 489 AA: 12367 MM: 6A13E319 CP0320.

Query Match 100.0%; Score 26; DB 9; Length 489;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STSC 5
 |||||
 Db 340 STSC 344

Search completed: June 22, 1999, 11:01:24
 Job time: 170 sec



Copyright (c) 1993 - 1998 CompuGen Ltd

OM protein - protein search, using sw model

Run on: Tue 22, 1999, 10:59:45 ; Search time 45.16 Seconds

2.972 Million cell updates/sec

Title: US-09-030-061-5

Sequence:

Scoring table: BIOSUM62

Searched: 74.15 segs, 26840296 hits, 4.4ps

Database : SwissProt_36:★

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is taken from analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description
1	26	100.0	326	1	AAP_PAT	P36647 ratius nov
2	26	100.0	789	1	ACOX_YEAST	P36533 saccharomyces
3	26	100.0	412	1	ESR2_BRAF	Q65150 brachydanio
4	26	100.0	2715	1	G156_PAPR	P13817 paramecium
5	26	100.0	33	1	GAED_RABR	P80396 rana rugosa
6	26	100.0	33	1	GAED_RABR	P80397 rana rugosa
7	26	100.0	509	1	HYAL_HUMAN	P38567 homo sapien
8	26	100.0	194	1	IL18_HUMAN	Q11116 homo sapien
9	26	100.0	192	1	IL18_MOUSE	P70380 mus musculi
10	26	100.0	160	1	IL18_PIG	Q10973 sus scrofa
11	26	100.0	194	1	IL18_RAT	P97636 rattus norv
12	26	100.0	830	1	LEH3_HUMAN	P08235 homo sapien
13	26	100.0	984	1	MCP_HUMAN	P44650 hemophilus
14	26	100.0	113	1	NAPF_HA1IN	P41393 shistosoma
15	26	100.0	720	1	NCA4_SCOP	P54332 dioscorea
16	26	100.0	752	1	NFT2_EPMF	P54332 dioscorea
17	26	100.0	502	1	PRIF_ECOLI	P07117 escherichia
18	26	100.0	502	1	PRIF_ECOLI	P10502 salmonella
19	26	100.0	245	1	PRPH_SALT	P17147 chlamydia
20	26	100.0	906	1	PRH1_HCVAA	P16782 human cyto
21	26	100.0	177	1	VR22_ASFB7	P23169 artisa
22	26	100.0	720	1	YD71_SCOP	P23169 artisa
23	26	100.0	840	1	YHT1_YEAST	P38835 saccharomy
24	26	100.0	126	1	YNR3_YEAST	P38835 saccharomy
25	26	100.0	126	1	YNR3_YEAST	P38835 saccharomy
26	26	100.0	126	1	YNR3_YEAST	P38835 saccharomy
27	26	100.0	973	1	YNR3_YEAST	P38835 saccharomy
28	26	100.0	217	1	YNR3_YEAST	P38835 saccharomy
29	26	100.0	1108	1	YNR3_YEAST	P38835 saccharomy
30	26	100.0	652	1	YNR3_YEAST	P38835 saccharomy
31	26	100.0	72	1	YNR3_YEAST	P38835 saccharomy
32	26	100.0	122	1	YNR3_YEAST	P38835 saccharomy
33	26	100.0	465	1	YNR3_YEAST	P38835 saccharomy
34	26	100.0	173	1	YNR3_YEAST	P38835 saccharomy
35	26	100.0	1260	1	YNR3_YEAST	P38835 saccharomy
36	26	100.0	1260	1	YNR3_YEAST	P38835 saccharomy
37	26	100.0	1260	1	YNR3_YEAST	P38835 saccharomy
38	26	100.0	1260	1	YNR3_YEAST	P38835 saccharomy
39	26	100.0	1260	1	YNR3_YEAST	P38835 saccharomy
40	26	100.0	1260	1	YNR3_YEAST	P38835 saccharomy
41	26	100.0	1260	1	YNR3_YEAST	P38835 saccharomy
42	26	100.0	1260	1	YNR3_YEAST	P38835 saccharomy
43	26	100.0	1260	1	YNR3_YEAST	P38835 saccharomy

RESULT						
						ALIGNMENTS
1	ID	AA3R_PAT	STANDARD	PST.	320 AA.	
AC	D28647:	063792:				
PT	DEC-1992 (REL. 24,					
DT	01-NOV-1997 (PEL. 35,					
DT	15-JUN-1998 (PEL. 36,					
DE	AENOSINFR A3 RECEPTOR (HOMER).					
GN	ADORA3.					
OS	RATTUS NORVEGICUS (PAT)					
CC	EXTRACTA; MURINA; CHOLESTA; VERTEBRA; EUMARCA; MAMMALIA;					
OC	EUTHERIA; RODENTIA.					
RN	[1]					
RP	SEQUENCE FROM N.A. AND CHARACTERIZATION.					
KC	TISSUE-BRAIN:					
RX	MEDLINE: 92366475.					
KA	CHAP GUY LUCY, J., LAKE M.E., THANSEN F.A., STEINE D.M., STRELL D.J.					
PL	PROC NATL ACAD SCI U S A 89:7473-7476(1992).					
RL	[2]					
RP	SEQUENCE FROM N.A.					
PC	SIPAIN-MISTAP: TISSUE-TESTIS:					
RX	MEDLINE: 91295122.					
RA	MEYERHOE W., MILLER-BROCKLIN R., RICHTER D.: FEBS LETT. 294:157-160(1991).					
EL	[3]					
RN						
RF	SEQUENCE FROM N.A.					
RC	TISSUE-BRAIN:					
RX	MEDLINE: 96196578. SAJIANI F.B.; KAYLE B.I.; DOMINGO P.C.; FIRESTEIN G.S.: FEBS LETT. 382:125-129(1996).					
CL	- FUNCTION: RECEPTOR FOR ADENOSINE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBITS ADENYLATE CYCLASE. POSSIBLE ROLE IN REPRODUCTION. CELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. - TISSUE SPECIFICITY: TESTES, PARTICULARLY IN SPERMATOZOYES AND SPERMATIDS BUT NOT IN SPERMATOGENIA. LOW LEVELS IN THE BRAIN. - DEVELOPMENTAL STAGE: EXPRESSED DURING SEPMATOGONESIS. - ALTERNATIVE PRODUCTS: TWO FORMS ARE PRODUCED BY ALTERNATIVE SPLICING.					
CC	- SIMILARITY: BELONGS TO FAMILY I OF G-PROTEIN COUPLED RECEPTORS.					
DR	EWBL: X59249: G56308: -					
DR	EWBL: M4152: C460332: -					
DR	EWBL: X92219: E213918: -					
DR	FIR: S11777: S17177.					
DR	FIR: M4152: A46152.					
TF	GSTR: GSE_0177: -					
GF	GCDR: GCR_0173: -					
GORB	GCR_1342: -					
HA	HOMOLOGY SEARCH: G-PROTEIN_RECEPTOR_1					
KK	G-PROTEIN COUPLED RECEPTOR SPANMEMBRANE CYTOPROTEIN: DIFFERENTIAL PALMITATE ALTERNATIVE SPLICING.					
KW	DOMAIN: 1					
FT	TRANSEM	17	32			
LMAIN	16	50	74			
FT	TRANSSEM	51	74			
FT	DOMAIN	75	86			
FT	TRANSSEM	77	105			
LMAIN	109	146				
FT	TRANSSEM	129	150			
LMAIN	122	172				
FT	TRANSSEM	169	400			
LMAIN	351	113				
FT	TRANSSEM	324	357			
FT	TRANSSEM	359	368			
LMAIN	287	466				
FT	CYTOLASMIC (POTENTIAL). CYTOPLASMIC (POTENTIAL). EXTRACELLULAR (POTENTIAL). EXTRACELLULAR (POTENTIAL). CYTOPLASMIC (POTENTIAL). CYTOPLASMIC (POTENTIAL). EXTRACELLULAR (POTENTIAL). CYTOPLASMIC (POTENTIAL). CYTOPLASMIC (POTENTIAL). CYTOPLASMIC (POTENTIAL).	320				

CC CYSTEINES, EXCEPT FOR FOUR HALF PERIODS. A VARIABLE PART OF 475
 CC RESIDUES COMPRISES 4 ALMOST IDENTICAL PERIODS IN THE MIDDLE OF THE
 CC PROTEIN.
 CC -1- EXPRESSION OF 3 PROTEIN OCCURS AT LOW TEMPERATURES (14-32
 CC DEGREES CELSIUS).
 CC -1- SIMILARITY: 98% TO THE ALLELIC FORM 1686 PROTEIN (P17053) IN
 CC PERIODIC STRUCTURE AND 80% IN VARIABLE DOMAIN IN THE MIDDLE OF
 CC THE PROTEIN.
 DR EMBL: X03893 (G578475).
 DR PIR: A23475, A23475.
 DR HSPD: P06620, A23475.
 KW SIGNAL: REPEAT: ANTIGEN: MEMBRANE: GPI-ANCHOR.
 FT SIGNAL 1 20
 FT CHAIN 21 2715 1566 SURFACE PROTEIN
 FT DOMAIN 106 2560 37 X 75 AA APPROXIMATE REPEATS.
 FT SPLIT 1 222 89% TO PARALLEL TO TETRAPEPTIDE A
 FT SEQUENCE 2715 AA: 272221 MW: 64955AA GPC32.

Query Match 100.0% Score 26; DB 1; Length 2715.
 Best Local Similarity 100.0% Pred. No. 3 Se-02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STISC 5
 DB 23 STISC 27

RESULT 5
 GAE2_RANRU STANDARD; PRI: 33 AA.
 AC P80396;
 DT 01-NOV-1994 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE GAEGRIN-2;
 OS RANA FUSCATA (FROG);
 OC FRYAVERGA METAZOA: CHORDATA: VERTEBRATA: TETRAPEPTIDE: AMPHIBIA: ANURA.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-SKIN;
 RX MEDLINE: 95091844.
 RA PARK J.M., JUNG J.-E., LEE B.-J.,
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 205:948-954(1994).
 CC -1- FUNCTION: HAS A NON-HEMOLYTIC ACTIVITY HAS A BROAD SPECTRUM OF
 CC ACTIVITY AGAINST BOTH GRAM POSITIVE AND GRAM NEGATIVE BACTERIA,
 CC FUNGI AND PROTOZOA.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- TISSUE SPECIFICITY: SKIN.
 CC -1- SIMILARITY: BELONGS THE PREVINCIN/ESULENTIN/TACROFIN/PRODOSIN
 CC FAMILY.
 KW AMPHIBIAN SKIN: ANTIBIOTIC.
 FT DISULFID 27
 FT SEQUENCE 33 AA: 3322 MW: 965297A GPC32;

Query Match 100.0% Score 26; DB 1; Length 33;
 Best Local Similarity 100.0% Pred. No. 7.3;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STISC 5
 DB 23 STISC 27

RESULT 6
 GAE2_RANRU STANDARD; PRI: 33 AA.
 AC P80397;
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 32, LAST SEQUENCE UPDATE)

DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE GAEGRIN-3;
 OS RANA FUSCATA (FROG);
 OC FRYAVERGA METAZOA: CHORDATA: VERTEBRATA: TETRAPEPTIDE: AMPHIBIA: ANURA.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-SKIN;
 RX MEDLINE: 95091844.
 RA PARK J.M., JUNG J.-E., LEE B.-J.,
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 205:948-954(1994).
 CC -1- FUNCTION: HAS A NON-HEMOLYTIC ACTIVITY. HAS A BROAD SPECTRUM OF
 CC ACTIVITY AGAINST BOTH GRAM POSITIVE AND GRAM NEGATIVE BACTERIA,
 CC FUNGI AND PROTOZOA.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- TISSUE SPECIFICITY: SKIN.
 CC -1- SIMILARITY: BELONGS THE PREVINCIN/ESULENTIN/TACROFIN/PRODOSIN
 CC FAMILY.
 KW AMPHIBIAN SKIN: ANTIBIOTIC.
 FT DISULFID 27
 FT SEQUENCE 33 AA: 3309 MW: A8160CPR GPC32;

Query Match 100.0% Score 26; DB 1; Length 33;
 Best Local Similarity 100.0% Pred. No. 7.3;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STISC 5
 DB 23 STISC 27

RESULT 7
 HVAL_HUMAN STANDARD; PRI: 509 AA.
 ID HVAL_HUMAN
 AC P38567;
 DT 01-OCT-1994 (REL. 30, CREATED)
 DT 01-OCT-1994 (REL. 40, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE HYALURONIDASE PROTECTOR (PC 3.2.1.35) (SPERM SUPPARE PROTEIN PG-20)
 DE (SPERM ADHESION MOLECULE 1).
 GN SPAM OR HYAL OR H420.
 OS HOMO SAPIENS (HUMAN);
 OC FRYAVERGA METAZOA: CHORDATA: VERTEBRATA: TETRAPEPTIDE: MAMMALIA:
 CC EUTHERIA: PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 PP SEQUENCE FROM N.A.
 RC TISSUE-TESTIS;
 RX MEDLINE: 94052105.
 RA LIN Y., KIMMEL T.H., MYLES D.G., FRIMARKOFF P.,
 RL FECHT N.M., ARAF S.H., ARAF A.,
 RN [2]
 RP SEQUENCE FROM N.A.
 PP SEQUENCE FROM N.A.
 RC TISSUE-TESTIS;
 RX MEDLINE: 94109604.
 RA GMAHEL M., SAGAN S., KETTER S., KREIL G.,
 RL FECHT N.M., ARAF S.H., ARAF A.,
 RN [3]
 RP SEQUENCE FROM N.A.
 PP SEQUENCE FROM N.A.
 RC TISSUE-TESTIS;
 RX MEDLINE: 96121393.
 RA JONES M.H., DAVEY P.M., APLIN H., AFFARA N.A.,
 RL GENOMICS 29:796-800(1995).
 CC -1- FUNCTION: INVOLVED IN SPERM-EGG ADHESION. UPON FERTILIZATION
 CC SPERM MUST PENETRATE A LAYER OF CORIUS CELLS THAT
 CC SUPPORTS THE EGG BEFORE REACHING THE ZONA PELLUCIDA. THE
 CC CORIUS CELLS ARE EMBEDDED IN A MATRIX CONTAINING HYALURONIC
 CC ACID WHICH IS HYALURONIC ACID. THIS PROTEIN AIDS IN
 CC PENETRATING THE LAYER OF CORIUS CELLS BY DIGESTING HYALURONIC
 CC ACID.
 CC -1- CATALYTIC ACTIVITY: RANDOM HYDROLYSIS OF 1,4-LINKAGES BETWEEN
 CC N-ACETYL-HEXA-D-DEOXYAMINE AND D-DEOXYRIBONATE RESIDUES IN
 CC HYALURONATE.

[illegible]

```

Query Match          100.0%  Score 26:  DB 1:  Length 192:
Best Local Similarity 100.0%  Pred. No. 34:
Matches             5:  Conservative  0:  Mismatches  0:  Tuples  0:  Gaps

```

2Y 1 STSC 5
 |||||
 LB 106 STSC 110

RESULT 10
 IL18_PIG
 IL18_PIG: STANFAC: PR1: 100 AA.
 AC 019073;
 DT 15-JUL-1998 (REL. 36, CREATED)
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 LT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE INTERLEUKIN-18 PRECURSOR (IL18) (INTERPEPON-GAMMA INDUCING FACTOR)
 DE (ILN-GAMMA-INDUCING FACTOR) (INTERLEUKIN-1 GAMMA) (IL-1 GAMMA)
 DE (FRAGMENT).
 DE IL18 OR IGIF.
 GN GN
 OS SUS SCROPA (PIG).
 OC PTERAPOTA METAZOA, CHORDATA, VERTEBRATA, TETRAPODA, MAMMALIA,
 EUMETAZOA, ARTIODACTYLIA.
 RN (1)
 RP SEQUENCE FROM N.A.
 RA POSS D.L. , MORTAUGH M.P.;


```

CC 1- DOMAIN COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
CC A PNA-TYPE DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
CC 1- SIMILARITY: RTIONS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
DR EMBL: M6801; G307166; -.
DR PIR: A29512; A29512.
DR HSSP: P06536; IGDC.
DR TRANSFAC: T00513; -.
DR MIM: 600983; -.
DR PROSITE: PS00031; NUCLEAR RECEPTOR 1.
KW PROSITE: TRANSSCRIPTION REGULATION; DNA-BINDING; NUCLEAR PROTEIN.
KW ZINC-FINGER; STEROID-BINDING.
FT DOMAIN 1 602 MODULATING.
FT DNA_BIND 603 668 C4-TYPE ZINC FINGERS (TW).
FT ZN_FING 603 623 C4-TYPE.
FT ZN_FING 639 663 C4-TYPE.
FT DOMAIN 669 732 HINGE.
FT DOMAIN 733 984 STEROID-BINDING.
SQ SEQUENCE 984 AA: 107067 MW: 98721940 CPC32.

Query Match 100.0% Score 26; DB 1; Length 984;
Best Local Similarity 100.0%; Pctd NO. 14e-02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 1 STISC 5
DB 152 STISC 156

RESULT 14
NAME_HAEIN STANDARD; PRT; 113 AA.
ID NAME_HAEIN STANDARD; PRT; 113 AA.
AC P44650;
DT 01-NOV-1995 (REL. 32, CREATED)
DI 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
ZI 01-NOV-1996 (REL. 32, LAST ANNOTATION UPDATE)
DE FERREDOXIN TYPE PROTEIN NAME_HAEIN HEMOLOGS.
CR NAME_HAEIN OR H10342.
OS HAEMOPHILUS INFLUENZAE.
OS POKKARYOTA: GACILICUTES: SNTOPACTERIA: FACULIA: (PNA) ANAEROBIC BACTERIA.
OC PASTEURILLACEAE.
NC 11.
RP SEQUENCE FROM N.A.
RC STRAIN-BD / KW20;
RX MEDLINE: 97450630.
RA FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON P.A., KINNESS E.F.,
RA KERVINAVE A.P., RUIT G.T., TOMR J.F., DOUGHERTY B.A., MERRICK J.M.,
RA MCKENNEY K., STUTON G., FITZGIBB W., FIELDS C.A., GOCAYNE J.D.,
RA SCOTT J.D., SHIPLEY R., LIU L.-I., GLODER A., KELLEY J.M.,
RA WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HERDLIN E.C., OTTIN M.D.,
RA UTTERBACK T.P., HANNA M.C., NICHEN D.T., SANDER G.M., BEAUGEN P.C.,
RA FINE L.D., FRITCHMAN J.T., PIERHANN T.T., GEORGIANN N.S.M.,
RA GUEHM C.L., MCLENNAN L.A., SMALL R.V., FRASER C.W., SMITH H.O.,
RA VENTER J.C.;
RA SCIENCE 269:496-512(1995).
CC 1- FUNCTION: INVOLVED IN ELECTRON TRANSFER.
CC 1- SIMILARITY: THE IRON-SULFUR CENTERS ARE SIMILAR TO THOSE OF
CC 'BACTERIAL-TYPE' 4FE-4S FERREDOXINS.
DR EMBL: U52719; G157313; -.
DR TIGR: H10342; -.
DR PROSITE: PS00199; 4FE4S FERREDOXIN; 1.
KW ELETTRON TRANSFER; IRON-SULFUR; 4FE-4S.
FT METAL 48 48 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
FT METAL 51 51 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
FT METAL 51 51 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
FT METAL 58 58 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
FT METAL 80 80 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
FT METAL 83 83 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
FT METAL 86 86 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
FT METAL 90 90 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
FT METAL 93 93 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
SQ SEQUENCE 113 AA: 107067 MW: 9920990 CPC32.

```

Query Match: 100.0%; Score 26; DB 1; Length 113;
 Best Local Similarity: 100.0%; Pred No: 21;
 Matches: 5; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 STRSC 5
 DB 17 STRSC 21

RESULT 15
 ND4_SCHPO STANDARD: PRT: 720 AA.
 ID ND4_SCHPO
 AC P41389;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DI 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DI 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE CELL DIVISION CONTROL PROTEIN ND4.
 GN ND4 OR SPAC310.01.
 OS SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
 CC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDGENE: 94129084.
 RA MIYAKE S., KISHINO N., SAWATIMA I., HIRAKAWA Y., ITOA T., SAITOH I.,
 RA YANAGIDA M.:
 RL MOL. BIOL. CELL 4:1003-1015(1993).
 RN [2]
 RP SEQUENCE OF 72-720 FROM N.A.
 RC STRAIN=9712;
 RA MURPHY J., HARRIS D., BARRETT R.G., PALANDREAN M.A., WALSH S.V.:
 RL SUBMITTED (FEB-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- FUNCTION: ROLE IN DNA REPLICATION AND ESSENTIAL FOR VIABILITY.
 CC -1- STRUCTURAL LOCATION: NUCLEAR (POTENTIAL).
 CC -1- SIMILARITY: BELONGS TO THE MCM FAMILY.
 DR EMBL: S68467; G545211; -;
 DR EMBL: E69260; E211200; -;
 DR PIR: A48723; A48723;
 DR PROSITE: PS20847; MCM_1; 1;
 DR PROSITE: PS20851; MCM_2; 1;
 KW TRANSCRIPTION REPLICATION; DNA-BINDING; NUCLEAR PROTEIN;
 KM DNA REPLICATION; CELL CYCLE; ATP-BINDING;
 FT DOMAIN 307 312 POLY-GLU.
 FT DOMAIN 322 329 MCM.
 FT NP_BIND 372 379 ATP (POTENTIAL).
 FT CONFLICT 461 461 A -> R (IN REF. 1).
 SO SEQUENCE 720 AA; 90099 MW; 22261458 CRC32;

Query Match: 100.0%; Score 26; DB 1; Length 720;
 Best Local Similarity: 100.0%; Pred No: 1,11e+02;
 Matches: 1; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 STRSC 5
 DB 154 STRSC 158

Search completed: June 22, 1999, 10:59:46
 Job time: 72 sec




```

C|Species: Mus musculus (house mouse)
C|Date: 31-Dec-1993 #sequence_revision 02-Jun-1994 #oxi_#ntype 1#-Sep-1994
C|Accession: S15661, S19108
R|Rutherford, M.N.; Kumar, A.; Nissim, A.; Chebath, J.; Williams, E.R.G.
N|Nucleic Acids Res. 19, 1977-1924, 1991
A|Title: The murine 2.5A synthetase locus: three distinct transcripts
A|Reference number: S15660, MIM-01932962
A|Accession: S15661
A|Molecule type: mRNA
A|Residues: 1-197, 8279
A|Cross reference: EMBL:X55982
R|Williams, B.
S|Submitted to the EMBL Data Library, September 1990
A|Reference number: S19108
A|Accession: S19108
A|Molecule type: mRNA
A|Residues: 1-175, 177-192 <MIL>
A|Cross reference: EMBL:X55982, NID:q49714, PID:q49715
C|Superfamily: G119(A) synthetase
C|Keywords: nucleotidyltransferase

Query Match          9.3%  Score 75.51  DB 2:  Length 192:
Best Local Similarity 23.2%  Prog. No. 2.67
Mismatch  42  Conserved  47  Mismatches  50  Incons  687  GAPS  47

  1  KLSVKNINQVIFDQGNHFFHMMT-----SQCPRNAFTFETSTKSGYRQNAV 62
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
  2  KVMGKVINLQTNLAFNQLINFSQYMAAVLMLDLAVLMAALINLQIPV 184
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
  3  TIVKQKVI-STISQENKTISEKMNPNQIKQKQNLIPQGVSPHNNKQGGSSV 12
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
  4  TIRISIRFVSNQNPQVILKELPETPKIKETSLTFMK-----HNNMYKSNAH 234
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

RESULT 11
146620
Sus scrofa prointerleukin-1 alpha mRNA, complete cds - pig
C|Species: Sus scrofa domestica (domestic pig)
C|Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #oxi_#ntype 0#-May-1997
C|Accession: I46620
R|Maliszewski, G.
N|Nucleic Acids Res. 14, 4282, 1990
A|Title: Nucleotide sequence of porcine interleukin-1 alpha
A|Reference number: I46620
A|Accession: I46620
A|Status: preliminary, translated from GR/EMBL/IDB:
A|Molecule type: mRNA
A|Residues: 1-270 <MAL>
A|Cross reference: EMBL:M47730, NID:q14602, PID:q14602
C|Superfamily: interleukin-1

```

Q: 121 EST/BLAST/BLAST 121
 Db 230 EST/BLAST/BLAST 240

RESULT 12

A: serine/threonine-specific protein kinase cot, 52K form - human
 A: serine/threonine-specific protein kinase cot, 52K form
 N: Contains: serine/threonine-specific protein kinase cot, 52K form
 C: Species: Homo sapiens (Man)
 C: Date: 07-Apr-1994 #sequence-revision 18-Nov-1994 #text-change 10-Jul-1998
 C: Accession: A48713; B48713; S31639
 J: Aoki, M.; Hamada, F.; Sugimoto, T.; Sumida, S.; Akiyama, T.; Toyoshima, K.
 J: Biol. Chem. 269: 22723-22732, 1993
 A: Title: The human cot protein-encoding gene encodes two protein serine/threonine kinases with
 A: Reference number: A48713; MIM:3404034
 A: Accession: A48713

A: Status: preliminary
 A: Molecule type: mRNA
 A: Residues: 1-457 AA's
 A: Experimental source: TCO-4 cells
 A: Note: Sequence identical with p12cat138 transfection
 A: Note: Sequence extracted from NCBI database (NCBI:138970, NCBI:138972)
 A: Accession: B48713
 A: Status: preliminary
 A: Molecule type: mRNA
 A: Residues: 30-457 AA's
 A: Experimental source: TCO-4 cells
 A: Note: sequence inconsistent with nucleotide translation
 A: Note: sequence extracted from NCBI database (NCBI:138970, NCBI:138972)
 A: Accession: B48713; M. Aarssen, S.A. Miki, T. McGovern, E.S.
 A: Title: A M. Chodis, M. Aarssen, S.A. Miki, T. McGovern, E.S.
 A: Description: A transforming gene isolated by expression cloning from Ewing's sarcoma
 A: Reference number: S31639
 A: Accession: S31639
 A: Status: preliminary
 A: Molecule type: mRNA
 A: Residues: 1-457 AA's
 A: Cross-references: EMBL:214138, NID:931244; PID:931245
 C: Superfamily: protein kinase homology
 C: Keywords: alternative initiator; proto-oncogene
 F: 138-388/Lowdell protein kinase homology <KIN>

Query Match 9.3% Score 75.5; DB 2; Length 467;
 Best Local Similarity 22.1%; Pred. No. 7.4;
 Matches 31; Conservative 25; Mismatches 39; Indels 45; Gaps 7;

Q: 13 FRNAGVFTTGNFFIFEMTSCF-----DNAPITF-----ISMV 52
 Db 333 RSNVSYIYIHKQAPLEAD-DCSPGRELLEASLERPNRPRAADLKHEALNP 391
 Q: 53 KDSPPRAVITVKCEITSLSCNK-TISFKENPNDIKD-----KSLITFOR 104
 Db 302 FETDPP-----QSLDSALIEPKPLSPKLELPENLADSSCTGSEEMLROR 442
 Q: 105 SVPCNCHNMGFESSYEYF 124
 Db 443 S-----LYIDLGLALGYF 455

RESULT 13

ret protein - chicken
 C: Species: Gallus gallus (chicken)
 C: Date: 10-Oct-1995 #sequence-revision 03-Nov-1995 #text-change 19-Dec-1997
 C: Accession: S57450
 R: Robertson, K.; Mason, J.
 R: Sub: 1993, 11; FMP: 1993 library June 1995
 A: Description: Expression of ret in the chicken embryo suggests roles in regionalisation
 A: Reference number: S57450
 A: Accession: S57450

A: Status: preliminary
 A: Molecule type: mRNA
 A: Residues: 1-1064 AA's
 A: Cross-references: EMBL:214949, NID:987041, FID:987042
 C: Superfamily: protein-tyrosine kinase ret; protein kinase homology
 C: Keywords: ATP
 F: 714-1004/Domain: protein kinase homology <KIN>
 F: 722-730/Region: protein kinase AII binding motif

Query Match 9.2% Score 75; DB 2; Length 1064;
 Best Local Similarity 22.4%; Pred. No. 22;
 Matches 38; Conservative 29; Mismatches 56; Indels 48; Gaps 7;

Q: 15 LNFVFTTGNFFIFEMTSCF-----DNAPITF-----ISMV 52
 Db 107 LSNVSYIYIHKQAPLEAD-DCSPGRELLEASLERPNRPRAADLKHEALNP 391
 Q: 75 SCENKTIKFNKPNPNIETKDIFFQSVPCNCHNMGFESSYEYF 129
 Db 152 SCENKTIKFNKPNPNIETKDIFFQSVPCNCHNMGFESSYEYF 129
 Q: 129 SCENKTIKFNKPNPNIETKDIFFQSVPCNCHNMGFESSYEYF 129
 Db 206 SCENKTIKFNKPNPNIETKDIFFQSVPCNCHNMGFESSYEYF 129

RESULT 14

proto-oncogene protein - mouse
 C: Species: Mus musculus (house mouse)
 C: Date: 02-Jul-1994 #sequence-revision 02-Jul-1994 #text-change 10-Jul-1993
 C: Accession: I49609
 R: Ohata, R.; Miyoshi, J.; Aoki, M.; Toyoshima, K.
 R: Jpn. J. Cancer Res. 84: 518-525, 1993
 A: Title: The murine cot proto-oncogene: genome structure and tissue-specific expression
 A: Reference number: I49609; MIM:93308016
 A: Accession: I49609
 A: Status: preliminary; translated from GB/EMBL/DBJ
 A: Molecule type: mRNA
 A: Residues: 1-467 AA's
 A: Cross-references: GenBank:U01709; NID:9296072; FID:9296073
 C: Genes: cot
 C: Superfamily: protein kinase homology
 F: 138-388/Lowdell protein kinase homology <KIN>

Query Match 9.2% Score 75; DB 2; Length 467;
 Best Local Similarity 21.0%; Pred. No. 8.2;
 Matches 29; Conservative 22; Mismatches 56; Indels 34; Gaps 6;

Q: 12 FRNAGVFTTGNFFIFEMTSCF-----DNAPITF-----ISMV 52
 Db 361 RSNVSYIYIHKQAPLEAD-DCSPGRELLEASLERPNRPRAADLKHEALNP 391
 Q: 72 SCENKTIKFNKPNPNIETKDIFFQSVPCNCHNMGFESSYEYF 129
 Db 402 SCENKTIKFNKPNPNIETKDIFFQSVPCNCHNMGFESSYEYF 129
 Q: 124 F 124
 Db 455 F 455

RESULT 15

hypothetical protein MG414 - Mycoplasma genitalium (SGC3)
 C: Species: Mycoplasma genitalium
 C: Date: 10-Nov-1995 #sequence-revision 10-Nov-1995 #text-change 13-Sep-1998
 C: Accession: H64245
 R: Fraser, C.M.; Goodyear, J.D.; White, O.; Adams, M.D.; Clayton, P.A.; Fleischmann, R.
 R: M. J. Friedman, D. Nguyen, D. O'Brien, T. R. Sastry, D. M. Phillips, C. A. Merrick,

GenCore version 4.5
Copyright (c) 1993 - 1998 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 22, 1999, 10:59:46 ; Search time 45.16 seconds

(without alignments) 93.311 Million cell updates/sec

Title: US-09-030-061-6

816

Perfect score:

816

XXXXXXXXXXXXXXXXXXXX

Scoring table:

BLOSUM62

Sequences: 74019 seqs, 26840295 residues

Database: SwissProt_36*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match Length	EB	ID	Description
1	816	100	1	IL18_HUMAN	Q14116 homo sapien
2	520	63	1	IL18_MOUSE	P70380 mus musculu
3	519.5	63	1	IL18_FAT	P97436 rattus norv
4	513	62	1	IL18_FIT3	Q13073 sus scrofa
5	513	62	1	IL18_FIT3	P18430 sus scrofa
6	81	9	1	IL18_FIT3	P04822 ovicolaquus
7	80.5	9	1	MSPI_MOUSE	P01027 mus musculu
8	76	6	1	MSPI_PLAYO	P13829 plasmidom
9	75	9	1	KCOI_MOUSE	Q07174 mus musculu
10	74.5	9	1	KCOI_HUMAN	Q13501 homo sapien
11	74.5	9	1	V413_MYOG	P47654 myoclasma
12	74.5	9	1	V413_MYOG	P47654 myoclasma
13	74	9	1	GENE_HUMAN	U02224 homo sapien
14	72.5	8	1	IL18_BOVIN	P08831 bos taurus
15	72.5	8	1	KCOI_HUMAN	Q01279 homo sapien
16	72	8	1	KCOI_HUMAN	Q01279 homo sapien
17	72	8	1	KCOI_HUMAN	Q01279 homo sapien
18	71.5	8	1	KCOI_HUMAN	Q01279 homo sapien
19	71.5	8	1	KCOI_HUMAN	Q01279 homo sapien
20	71.5	8	1	KCOI_HUMAN	Q01279 homo sapien
21	71	8	1	KCOI_HUMAN	Q01279 homo sapien
22	70.5	8	1	KCOI_HUMAN	Q01279 homo sapien
23	70.5	8	1	KCOI_HUMAN	Q01279 homo sapien
24	70.5	8	1	KCOI_HUMAN	Q01279 homo sapien
25	70.5	8	1	KCOI_HUMAN	Q01279 homo sapien
26	70.5	8	1	KCOI_HUMAN	Q01279 homo sapien
27	70	8	1	KCOI_HUMAN	Q01279 homo sapien
28	70	8	1	KCOI_HUMAN	Q01279 homo sapien
29	70	8	1	KCOI_HUMAN	Q01279 homo sapien
30	70	8	1	KCOI_HUMAN	Q01279 homo sapien
31	70	8	1	KCOI_HUMAN	Q01279 homo sapien
32	70	8	1	KCOI_HUMAN	Q01279 homo sapien
33	70	8	1	KCOI_HUMAN	Q01279 homo sapien
34	70	8	1	KCOI_HUMAN	Q01279 homo sapien
35	70	8	1	KCOI_HUMAN	Q01279 homo sapien
36	70	8	1	KCOI_HUMAN	Q01279 homo sapien
37	70	8	1	KCOI_HUMAN	Q01279 homo sapien
38	70	8	1	KCOI_HUMAN	Q01279 homo sapien
39	70	8	1	KCOI_HUMAN	Q01279 homo sapien
40	70	8	1	KCOI_HUMAN	Q01279 homo sapien
41	70	8	1	KCOI_HUMAN	Q01279 homo sapien
42	70	8	1	KCOI_HUMAN	Q01279 homo sapien
43	70	8	1	KCOI_HUMAN	Q01279 homo sapien
44	70	8	1	KCOI_HUMAN	Q01279 homo sapien
45	70	8	1	KCOI_HUMAN	Q01279 homo sapien

44 67.5 8.3 1114 1 RB18_YEAST

Q12749 saccharomy

P01420 saccharo

ALIGNMENTS

Result	ID	IL18_HUMAN	STANDARD	PRT	193 AA
1	AC	Q14116			
2	DT	15-JUL-1998 (REL. 36) CREATED			
3	DT	15-JUL-1998 (REL. 36) LAST SEQUENCE UPDATE			
4	DT	15-JUL-1998 (REL. 36) LAST ANNOTATION UPDATE			
5	DE	INTERFERON-18 PEPTIDE (IL-18) (INTERFERON-GAMMA INDUCING FACTOR)			
6	DE	(IFN-GAMMA-INDUCING FACTOR) (INTERFERON-1 GAMMA) (IL-1 GAMMA)			
7	GN	IL18 OR IGIF			
8	GN	HOMO SAPIENS (HUMAN)			
9	OC	EUROPEAN: METAZOA: CHORDATA: VERTEBRATA: EUMETAZOA: MAMMALIA:			
10	OC	EUROPEAN: PRIMATES			
11	OC	EUROPEAN: PRIMATES			
12	OC	EUROPEAN: PRIMATES			
13	OC	EUROPEAN: PRIMATES			
14	OC	EUROPEAN: PRIMATES			
15	OC	EUROPEAN: PRIMATES			
16	OC	EUROPEAN: PRIMATES			
17	OC	EUROPEAN: PRIMATES			
18	OC	EUROPEAN: PRIMATES			
19	OC	EUROPEAN: PRIMATES			
20	OC	EUROPEAN: PRIMATES			
21	OC	EUROPEAN: PRIMATES			
22	OC	EUROPEAN: PRIMATES			
23	OC	EUROPEAN: PRIMATES			
24	OC	EUROPEAN: PRIMATES			
25	OC	EUROPEAN: PRIMATES			
26	OC	EUROPEAN: PRIMATES			
27	OC	EUROPEAN: PRIMATES			
28	OC	EUROPEAN: PRIMATES			
29	OC	EUROPEAN: PRIMATES			
30	OC	EUROPEAN: PRIMATES			
31	OC	EUROPEAN: PRIMATES			
32	OC	EUROPEAN: PRIMATES			
33	OC	EUROPEAN: PRIMATES			
34	OC	EUROPEAN: PRIMATES			
35	OC	EUROPEAN: PRIMATES			
36	OC	EUROPEAN: PRIMATES			
37	OC	EUROPEAN: PRIMATES			
38	OC	EUROPEAN: PRIMATES			
39	OC	EUROPEAN: PRIMATES			
40	OC	EUROPEAN: PRIMATES			
41	OC	EUROPEAN: PRIMATES			
42	OC	EUROPEAN: PRIMATES			
43	OC	EUROPEAN: PRIMATES			
44	OC	EUROPEAN: PRIMATES			
45	OC	EUROPEAN: PRIMATES			

Query Match
Best Local Similarity 19.4%
Matched 33, Unmatched 36, Mismatches 75, Indels 26, Gaps 7,
Score 79, DB 1, Length 1772

Query Match
Best Local Similarity 19.4%
Matched 33, Unmatched 36, Mismatches 75, Indels 26, Gaps 7,
Score 79, DB 1, Length 1772

Query Match
Best Local Similarity 19.4%
Matched 33, Unmatched 36, Mismatches 75, Indels 26, Gaps 7,
Score 79, DB 1, Length 1772

Query Match
Best Local Similarity 19.4%
Matched 33, Unmatched 36, Mismatches 75, Indels 26, Gaps 7,
Score 79, DB 1, Length 1772

Query Match
Best Local Similarity 19.4%
Matched 33, Unmatched 36, Mismatches 75, Indels 26, Gaps 7,
Score 79, DB 1, Length 1772

Query Match
Best Local Similarity 19.4%
Matched 33, Unmatched 36, Mismatches 75, Indels 26, Gaps 7,
Score 79, DB 1, Length 1772

Query Match
Best Local Similarity 19.4%
Matched 33, Unmatched 36, Mismatches 75, Indels 26, Gaps 7,
Score 79, DB 1, Length 1772

Query Match
Best Local Similarity 19.4%
Matched 33, Unmatched 36, Mismatches 75, Indels 26, Gaps 7,
Score 79, DB 1, Length 1772

DB 905 PIGVIRINUSVIRUS... (KININ)ELUAV... (AN)ENINMEDI... EN 956
 CG 120 EPITELIAL... (EPITELIAL)ENMED 117
 DB 951 COTLEFAS... (NON)ENFENENKSD 981

RESULT 13
 GENE_HUMAN
 ID GENE_HUMAN STANDARD PRT: 2663 AA
 AC 002231.
 DI 01-JUL-1993 (REL. 26, CREATED)
 DT 01-FEB-1995 (REL. 26, LAST SEQUENCE UPDATE)
 DT 01-NOV-1996 (REL. 32, LAST ANNOTATION UPDATE)
 EF CENTROMERIC PROTEIN F (CBPF-PROTEIN)
 GN CENPE
 OS HOMO SAPIENS (HUMAN)
 OC EUKARYOTA: METAZOA: VERTEBRATA: MAMMALIA:
 NC EUTHERIA: PRIMATES
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 9302422.
 RA LEN 100, DI 01, SCHAP B.L., SZILAK I., CIEPIAND D.W.
 RL NATURE 350:447-450 (1992)
 RN (2)
 RP CHARACTERIZATION
 RX MEDLINE: 9314785.
 RA THROMER D.A., JOHAN M.A., SCHAP B.L., YEN I.J., WILSON L.
 RL EMBO J. 14:916-926 (1995).
 CC -1- FUNCTION: KINOS-END DIRECTED MICROTUBULE MOTOR, PROBABLE
 KININ-ROBE MOTOR ACCUMULATES JUST BEFORE MITOSIS AT THE G2 PHASE
 OF THE CELL CYCLE. PROBABLY IMPORTANT FOR CHROMOSOME MOVEMENT
 AND/OR SPINDLE ELONGATION.
 CC -1- SUBCELLULAR LOCATION: ASSOCIATES WITH KINOCOPES DURING
 CONGRESSION, RELOCATES TO THE SPINDLE MIDZONE AT ANAPHASE, AND IS
 QUANTITATIVELY DISCARDED AT THE END OF THE CELL DIVISION
 CC -1- SIMILARITY: BELONGS TO THE KININ-LIKE PROTEIN FAMILY.
 DR EMBL: 2150051: G298651.
 DR PIR: S02231: S02231.
 DR MIM: 117143.
 DR PROSITE: PROSITE: KININ_MOTOR_DOMAIN: 1.
 DR PROSITE: PROSITE: KININ_MOTOR_DOMAIN: 1.
 KW MOTOR PROTEIN; CELL DIVISION; ATP-BINDING; COILED COIL; MITOSIS;
 KW CELL CYCLE; CENTROMERE.
 FT DOMAIN 1 336
 FT DOMAIN 346 2471
 FT DOMAIN 2472 2663
 FT BINDING 86
 FT SEQUENCE 1000 AA: 311227 MW: 341502.32 Da

Query Match 9.1%, Score 74, OR 1, Length 2663.
 Best Local Similarity 20.68, Pred. No. 68, Mismatches 72, Indels 30, Gaps 7
 Matches 300, Conserved 350

DB 4 KININ... (KININ)ELUAV... (AN)ENINMEDI... EN 956
 CG 120 EPITELIAL... (EPITELIAL)ENMED 117
 DB 951 COTLEFAS... (NON)ENFENENKSD 981

DB 60 MAVIN... (KININ)ELUAV... (AN)ENINMEDI... EN 956
 CG 120 EPITELIAL... (EPITELIAL)ENMED 117
 DB 951 COTLEFAS... (NON)ENFENENKSD 981

DB 468 AVIN... (KININ)ELUAV... (AN)ENINMEDI... EN 956
 CG 120 EPITELIAL... (EPITELIAL)ENMED 117
 DB 951 COTLEFAS... (NON)ENFENENKSD 981

DB 120 YECYEL... (KININ)ELUAV... (AN)ENINMEDI... EN 956
 CG 120 EPITELIAL... (EPITELIAL)ENMED 117
 DB 951 COTLEFAS... (NON)ENFENENKSD 981

DB 1026 TITTA... (KININ)ELUAV... (AN)ENINMEDI... EN 956
 CG 120 EPITELIAL... (EPITELIAL)ENMED 117
 DB 951 COTLEFAS... (NON)ENFENENKSD 981

RESULT 14
 ILIA_BOVIN
 ID ILIA_BOVIN STANDARD PRT: 268 AA
 AC 002231.
 DI 01-NOV-1996 (REL. 09, CREATED)

DI 01-NOV-1996 (REL. 09, LAST SEQUENCE UPDATE)
 DT 01-NOV-1996 (REL. 32, LAST ANNOTATION UPDATE)
 GN INTELLEKTIN-1 ALPHA (INTELLEKTIN-1)
 OS BOV TAPROS (BOVINE)
 OC EUKARYOTA: METAZOA: VERTEBRATA: MAMMALIA:
 NC EUTHERIA: ARTIODACTYLA
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 8901690.
 RA LEN 318, DI 01, FARGES G.M., TAMMAN M., GRAY P.W.
 RL NUCLEIC ACIDS RES. 16:9053-9053 (1988).
 RN (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 8918642.
 RA MALISZEWSKI G.R., BAKER F.E., SCHENGEN M.A., DAVIS R.S., JOHAN M.A.
 RL M.L. 10000: 5449-447 (1998).
 CC -1- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
 THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
 MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
 CC -1- IDENTIFIED AS ENDOTOXIN-PRODUCING, AND ARE REPORTED TO STIMULATE
 THE RELEASE OF PRO-INFLAMMATORY AND COLLAGENASE FROM SYNTHETIC CELLS.
 CC -1- SUBUNIT: MONOMER.
 CC -1- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
 AMINO-TERMINUS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
 CC -1- THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE PRECURSOR
 SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS OR IS
 SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
 SECRETORY PROTEINS.
 CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
 DR EMBL: M21937: G162227.
 DR EMBL: M32497: G445737.
 DR EMBL: M37210: G163199.
 DR PIR: J00064: J00064.
 DR PIR: S01379: S01379.
 DR HSSP: P01583: IITA.
 DR PROSITE: PROSITE: INTERLEUKIN_1.
 KW CYTOKINE; MACROPHAGE; MITOGEN; INFLAMMATORY RESPONSE; PROGEN.
 FT PROPEP 1 112
 FT GRAIN 113 268
 FT CARBOHYD 141 141
 FT SEQUENCE 268 AA: 30833 MW: 80433.34 Da

Query Match 9.94%, Score 72.7, OR 1, Length 268.
 Best Local Similarity 20.68, Pred. No. 68, Mismatches 72, Indels 30, Gaps 7
 Matches 270, Conserved 350

DB 8 KININ... (KININ)ELUAV... (AN)ENINMEDI... EN 956
 CG 120 EPITELIAL... (EPITELIAL)ENMED 117
 DB 951 COTLEFAS... (NON)ENFENENKSD 981

DB 63 TIV... (KININ)ELUAV... (AN)ENINMEDI... EN 956
 CG 120 EPITELIAL... (EPITELIAL)ENMED 117
 DB 951 COTLEFAS... (NON)ENFENENKSD 981

DB 183 TIR... (KININ)ELUAV... (AN)ENINMEDI... EN 956
 CG 120 EPITELIAL... (EPITELIAL)ENMED 117
 DB 951 COTLEFAS... (NON)ENFENENKSD 981

DB 121 BOY... (KININ)ELUAV... (AN)ENINMEDI... EN 956
 CG 120 EPITELIAL... (EPITELIAL)ENMED 117
 DB 951 COTLEFAS... (NON)ENFENENKSD 981

DB 239 TIT... (KININ)ELUAV... (AN)ENINMEDI... EN 956
 CG 120 EPITELIAL... (EPITELIAL)ENMED 117
 DB 951 COTLEFAS... (NON)ENFENENKSD 981

RESULT 15
 KOTI_HUMAN
 ID KOTI_HUMAN STANDARD PRT: 467 AA
 AC P41279.
 DI 01-FEB-1995 (REL. 31, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 EF 004 PRO-INFLAMMATORY SPONTANEOUSLY-INDUCED KININ (FC 3.7, 1.1-)
 GN (C-001) (KININ)ELUAV... (AN)ENINMEDI... EN 956

[illegible]

GenBank version 4.5
Copyright (c) 1998 - 1998 CompuGen Ltd.

OM proteins : protein search using sw model

Run on : 1999-11-01 14:24 Search time 83.17 seconds
(without alignments)
104.143 Million cell updates/sec

File : US-09-030-061-6

Sequence : 1 YFCKLESLVSNINPV... LKREDELQDPRSTWVQNEED 157

Scoring table : P1-SW62

Searched : 180763 seqs, 55169189 residues

Database :

SPREBEL-8:
1: SP_fungi:
2: SP_human:
3: SP_invertebrate:
4: SP_mammal:
5: SP_mhc:
6: SP_oranella:
7: SP-phage:
8: SP-plant:
9: SP_bacteria:
10: SP_fodentia:
11: SP_virus:
12: SP_vertebrate:
13: SP_unclassified:
14: SP_archaea:

Pred No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length	TP	FP	Test: P1: P2
1	806	98.0	193	2	0.75599	0.75599 homo sapien
2	775	97.3	194	19	0.88749	0.88749 caenorhabdi
3	80.5	11.1	270	1	0.43031	0.43031 schistosom
4	81.5	10.4	381	1	0.43031	0.43031 schistosom
5	81.5	10.0	617	3	0.25986	0.25986 plasmodium
6	80.5	9.9	666	4	0.44500	0.44500 plasmodium
7	80	9.8	447	12	0.90681	0.90681 gallus gall
8	79	9.7	452	3	0.77743	0.77743 caenorhabdi
9	78	9.6	473	3	0.16673	0.16673 caenorhabdi
10	77.5	9.5	270	4	0.28495	0.28495 caenorhabdi
11	77.5	9.5	1251	12	0.91365	0.91365 coturnix co
12	76.5	9.4	425	3	0.90390	0.90390 caenorhabdi
13	76	9.3	632	8	0.80569	0.80569 arabidopsis
14	75	9.3	747	8	0.88293	0.88293 arabidopsis
15	75.5	9.3	467	2	0.14375	0.14375 homo sapien
16	75.5	9.3	270	4	0.77743	0.77743 caenorhabdi
17	75.5	9.3	192	10	0.60856	0.60856 mus musculu
18	75	9.2	1183	3	0.18080	0.18080 caenorhabdi
19	75	9.2	445	12	0.57510	0.57510 scylleriin
20	75	9.2	1094	12	0.90681	0.90681 gallus gall
21	74.5	9.1	1930	2	0.22699	0.22699 caenorhabdi
22	74.5	9.1	137	3	0.77077	0.77077 plasmodium
23	74.5	9.1	351	3	0.83393	0.83393 liponema p
24	74	9.1	270	4	0.46613	0.46613 felis silve
25	74	9.1	371	10	0.76458	0.76458 mus musculu
26	74	9.1	457	10	0.63552	0.63552 rattus norv
27	74	9.1	970	10	0.88821	0.88821 mus musculu
28	73.5	9.0	475	3	0.16673	0.16673 caenorhabdi
29	74.5	9.0	896	4	0.24964	0.24964 mycoplasma

ALIGNMENTS

RESULT	ID	Score	Query Match	Length	TP	FP	Test: P1: P2
1	0.75599	98.0	193	2	0.75599	0.75599	homo sapien
2	0.88749	97.3	194	19	0.88749	0.88749	caenorhabdi
3	0.43031	11.1	270	1	0.43031	0.43031	schistosom
4	0.43031	10.4	381	1	0.43031	0.43031	schistosom
5	0.25986	10.0	617	3	0.25986	0.25986	plasmodium
6	0.44500	9.9	666	4	0.44500	0.44500	plasmodium
7	0.90681	9.8	447	12	0.90681	0.90681	gallus gall
8	0.77743	9.7	452	3	0.77743	0.77743	caenorhabdi
9	0.16673	9.6	473	3	0.16673	0.16673	caenorhabdi
10	0.28495	9.5	270	4	0.28495	0.28495	caenorhabdi
11	0.91365	9.5	1251	12	0.91365	0.91365	coturnix co
12	0.90390	9.4	425	3	0.90390	0.90390	caenorhabdi
13	0.80569	9.3	632	8	0.80569	0.80569	arabidopsis
14	0.88293	9.3	747	8	0.88293	0.88293	arabidopsis
15	0.14375	9.3	467	2	0.14375	0.14375	homo sapien
16	0.77743	9.3	270	4	0.77743	0.77743	caenorhabdi
17	0.60856	9.2	1183	3	0.60856	0.60856	mus musculu
18	0.18080	9.2	1094	12	0.18080	0.18080	caenorhabdi
19	0.57510	9.2	445	12	0.57510	0.57510	scylleriin
20	0.90681	9.2	1094	12	0.90681	0.90681	gallus gall
21	0.22699	9.1	1930	2	0.22699	0.22699	caenorhabdi
22	0.77077	9.1	137	3	0.77077	0.77077	plasmodium
23	0.83393	9.1	351	3	0.83393	0.83393	liponema p
24	0.46613	9.1	270	4	0.46613	0.46613	felis silve
25	0.76458	9.1	371	10	0.76458	0.76458	mus musculu
26	0.63552	9.1	457	10	0.63552	0.63552	rattus norv
27	0.88821	9.1	970	10	0.88821	0.88821	mus musculu
28	0.16673	9.0	475	3	0.16673	0.16673	caenorhabdi
29	0.24964	9.0	896	4	0.24964	0.24964	mycoplasma

DB 287 --LKMEALKEK3VLDPDYVBNENNKKMTLLD 320

RESULT 6
 AC 084500 PRELIMINARY: PRT: 866 AA.
 AC 084500:
 DI 01-NOV-1998 (TREMELBEL 02, CREATED)
 DI 01-NOV-1998 (TREMELBEL 02, LAST SEQUENCE UPDATE)
 DI 01-NOV-1998 (TREMELBEL 08, LAST ANNOTATION UPDATE)
 DE DNA PRIMERASE 1
 GN POLA.
 OS CHLAMYDIA TRACHOMATIS.
 OC BACTERIA: CHLAMYDIALES: CHLAMYDIACEAE: CHLAMYDIA.
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=EWING 100X
 RA STEPHENS P S, KALMAN S, LAMMEL C J, FAN J, MAPATHE P, ARAVIND L,
 RA MITCHELL W P, OLINGER L, TATISOV P L, ZHAO Q, KOONIN E V,
 RA DAVIS R W:
 PT "Genome Sequence of an Obligate Intracellular Pathogen of Humans:
 PT Chlamydia trachomatis".
 RC SCIENCE 0:0-0(1998).
 RN
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=EWING-3/EX:
 RA STEPHENS P S, KALMAN S, LAMMEL C J, FAN J, MAPATHE P, ARAVIND L,
 RA MITCHELL W P, OLINGER L, TATISOV P L, ZHAO Q, KOONIN E V,
 RA DAVIS R W:
 FL "Genome Sequence of an Obligate Intracellular Pathogen of Humans:
 DR EMBL: AEO01223: G3289292: -
 SQ SEQUENCE 866 AA: 96583 MW: 5088000A CRC32:

Query Match 9.84: Score 80.5; DB 9; Length 866;
 Best Local Similarity 26.4%; Pred. No. 23;
 Matches 45; Conservative 29; Mismatches 29; Indels 45; Gaps 9

QY 1 YKSTKTSKSVIRNNGVFI...TQGNRTFEEMTD...-----STGDNAPHTIFII 49
 DB 441 YKSLAKKIKATK...YTFVLEKSKLCEIYVHQH EAVIYFNER-----V 496
 QY 50 SMVTSKTFEYAV...ITVYCKEIKS...TSCENKITSFEMN-----V 91
 DB 447 GVFSTSS--GAVIFRTITFEELEKSEIYVLCWCEMNISFSLSTIYVQSGIFVEK 444
 QY 92 TKTAKST 100
 DB 545 AKSTKAEV 553

RESULT 7
 AC 090681 PRELIMINARY: PRT: 2470 AA.
 AC 090681:
 DI 01-NOV-1998 (TREMELBEL 01, CREATED)
 DI 01-NOV-1998 (TREMELBEL 01, LAST SEQUENCE UPDATE)
 DI 01-NOV-1998 (TREMELBEL 08, LAST ANNOTATION UPDATE)
 DE CATION-INDEPENDENT MANNOSE-6-PHOSPHATE RECEPTOR
 OS GALLUS GALLUS (CHICKEN).
 OS FRAXIPETIA METATA (HUMANIA VERTEBRATA): ANCHOROPRIA, AVES.
 OC NEOGNATHAE: GALLIFORMES: PHASIANIDAE: PHASIANINAE: GALLUS.
 RN
 RP SEQUENCE FROM N.A.
 RC MEDLINE 2600469.
 RA ZHOU M, MA Z, SUY W S:
 PT "Cloning and expression of the cDNA of chicken cation-independent
 PT mannose-6-phosphate receptor".
 RI PRCG MTT, ACAT SCI N S A 32 4762-4766(1995).
 DR EMBL: U35037: G1019119: -
 DR PFAM: PF00040: fn2: 1.
 DR PFAM: PF00579: C1MR_repeat: 13.
 DR SEQUENCE 2470 AA: 27645 MW: 6086076 CRC32:

Query Match 9.84: Score 80; DB 12; Length 2470;
 Best Local Similarity 25.9%; Pred. No. 90;
 Matches 45; Conservative 30; Mismatches 51; Indels 48; Gaps 12;

QY 4 KIESLSVTPNI ND---GVIFTEGNNPFFETMTISGPNAPR---IF--SMK----- 54
 DB 1457 KIESPELIMAEI--EYSLWFLMAACP-LKSNV--NDGPNVNNVIGLHFLDLSAKESQY 1515
 QY 54 ---SSPP-----GMVATI-----SVKCEYV--HSPN--IS--LKEK 86
 DB 1516 IITFSNKPFIIN--AKASSQANSAVAVIHPKTLNANLSLILYEVVLEKIVELG 1575
 QY 87 ND-PNINKT-KSOTIFPQSVPHNK---MPESSSYPRF-----LAPPE 130
 DB 1576 IGVPIIKKPSYSPVQKVASLSSAPVLSPEDEIOTISYPSWISLAVLE 1529

RESULT 8
 AC 025249 PRELIMINARY: PRT: 452 AA.
 AC 025249:
 DI 01-JAN-1998 (TREMELBEL 05, CREATED)
 DI 01-JAN-1998 (TREMELBEL 05, LAST SEQUENCE UPDATE)
 DI 01-NOV-1998 (TREMELBEL 08, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL 52.7 KD PROTEIN.
 GN HPO508.
 OS HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).
 OC BACTERIA: B. DEBARTYRA: BIFIDION SUCRISISTR: BIFIDOBACTERIACEAE:
 OC HELICOBACTER.
 RN
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=26695.
 RC MEDLINE: 97394467.
 RA TOMB J P, WHITE C, KERVAVAGE A P, CLAYTON R A, SUTTON G G,
 RA FITZGERALD P D, KETCHUM K A, KLEIN R E, JILL S, JOHNSON B A,
 RA NELSON K, QUACKENBUSH J, ZHOU L, KIRKNESS E F, PETERSON S,
 RA NELSON R, FITZGERALD L M, LEE N, ADAMS M D, HICKER E K,
 RA HOPD T E, GUYANE J D, WILHELM I K, FLEISCH J T, PETER J M,
 RA COTTON M D, WEIDMAN J M, FUJII G, ROMAN G, WATNEY L, WALLIN E,
 RA HAYES W S, BOBOLAVSKI M, KAP P D, SMITH H O, HANSEN J M,
 RA VENTER J C:
 PT "The 52.7 kDa subunit of the gastric pathogen Helicobacter
 PT pylori (published extratum appears in Nature 1997 Sep
 RI 371:289(6649):412)."
 RL NATURE 388:539-547(1997).
 DR EMBL: AEO00565: G2213524: -
 DR TIGR: HPO508: -
 KW HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 452 AA: 5065 MW: 7610000 CRC32:

Query Match 9.74: Score 79; DB 9; Length 452;
 Best Local Similarity 24.8%; Pred. No. 14;
 Matches 49; Conservative 3; Mismatches 46; Indels 48; Gaps 4

QY 4 GAVINLNDV--FTG--FLEMTSCNLNFIHISMKFQCT------- 59
 DB 106 IYV--VNNDA HIAEKELEYEIVANININISLIVINLNLK--ANLAVAN 103
 QY 59 -GMATISVCKEIKISGSCN-KIISFEMNPINIKKDIIFQFVGHQ---NK 112
 DB 164 YSVYIVITININISLIEHEIEREL---TISVTKSTFEE--VDIYVQVQK 219
 QY 112 MFESSSYEDF---LACEKELFLLEKDELKSLKIMTVQK 156
 DB 220 IYV--VNNDA IYV--VNNDA IYV--VNNDA IYV--VNNDA IYV--VNNDA 156

RESULT 9
 016673

[illegible]

01-NOV-1998 (PRELIMINARY) 08, LAST ANNOTATION UPDATE)
 DE SIMILARITY TO A CHOC-CLASS ZINC FINGER
 GN B6432.9
 OS CAENORHABDITIS ELEGANS
 OC EPIKAROTIA METACODA NEMATODA SEPTENTRIONIA PHAROTIA PHAROTIDA
 OC RHABDITIA METACODA NEMATODA SEPTENTRIONIA PHAROTIA PHAROTIDA
 RN 111
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2
 RX MEDLINE: 94150718
 RA WILSON R., ANDERSON K., BAYNES C., BERKS M., BONFIELD J.,
 RA PRITTON T., CONNELL M., DAVIES T., DOWDER J., GUTSON A., GRAYSON M.,
 RA DAVIS J., DAVIES T., DAVIES T., DAVIES T., DAVIES T., DAVIES T.,
 RA HASTING T., HILLIER L., JEFF M., JOHNSON L., JONES M., KERSHAW J.,
 RA KRISTEN J., LASTER N., LATREILLE P., LIGHTNING J., LLOYD C.,
 RA MONTGOMERY A., MONTGOMERY P., MONTGOMERY P., MONTGOMERY P.,
 RA PIERCE L., PIERCE A., PIERCE A., PIERCE A., PIERCE A., PIERCE A.,
 RA SONNHAMMER E., STADEN P., STURTON J., THIEPPE-MIES J., THOMAS K.,
 RA VAUDIN M., VAUGHAN K., WATKINSON P., WATSON A., WEINSTOCK L.,
 RA WILKINSON-SPOAT J., WOLDMAN P.
 RI "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RI elegans." 368132-38(1994).
 RL NATURE 368:32-38(1994).
 RN 121
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2
 RA HENKHAUS J., WOLDMAN P.
 RI SUBMITTED (CAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN 131
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2
 RA WATKINSON P.
 RI SUBMITTED (SEP-1998) TO EMBL/GENBANK/DBJ DATA BANKS
 DR EMBL: 080836, 01207142, 1
 DR PRAM, PROTEIN 7, 080836, 1
 SO SQUIDROTE 127 AA 199808 PRO322

Query Match 3.44 Score 76.5, DB 3, Length 425
 Best Local Similarity 19.74, Pred. No. 22
 Matches 46 Conservative 29 Mismatches 41 Totals 77 Gaps 6

01-NOV-1998 (PRELIMINARY) 08, LAST ANNOTATION UPDATE)
 DE SIMILARITY TO A CHOC-CLASS ZINC FINGER
 GN B6432.9
 OS CAENORHABDITIS ELEGANS
 OC EPIKAROTIA METACODA NEMATODA SEPTENTRIONIA PHAROTIA PHAROTIDA
 OC RHABDITIA METACODA NEMATODA SEPTENTRIONIA PHAROTIA PHAROTIDA
 RN 111
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2
 RX MEDLINE: 94150718
 RA WILSON R., ANDERSON K., BAYNES C., BERKS M., BONFIELD J.,
 RA PRITTON T., CONNELL M., DAVIES T., DOWDER J., GUTSON A., GRAYSON M.,
 RA DAVIS J., DAVIES T., DAVIES T., DAVIES T., DAVIES T., DAVIES T.,
 RA HASTING T., HILLIER L., JEFF M., JOHNSON L., JONES M., KERSHAW J.,
 RA KRISTEN J., LASTER N., LATREILLE P., LIGHTNING J., LLOYD C.,
 RA MONTGOMERY A., MONTGOMERY P., MONTGOMERY P., MONTGOMERY P.,
 RA PIERCE L., PIERCE A., PIERCE A., PIERCE A., PIERCE A., PIERCE A.,
 RA SONNHAMMER E., STADEN P., STURTON J., THIEPPE-MIES J., THOMAS K.,
 RA VAUDIN M., VAUGHAN K., WATKINSON P., WATSON A., WEINSTOCK L.,
 RA WILKINSON-SPOAT J., WOLDMAN P.
 RI "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RI elegans." 368132-38(1994).
 RL NATURE 368:32-38(1994).
 RN 121
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2
 RA HENKHAUS J., WOLDMAN P.
 RI SUBMITTED (CAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN 131
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2
 RA WATKINSON P.
 RI SUBMITTED (SEP-1998) TO EMBL/GENBANK/DBJ DATA BANKS
 DR EMBL: 080836, 01207142, 1
 DR PRAM, PROTEIN 7, 080836, 1
 SO SQUIDROTE 127 AA 199808 PRO322

01-NOV-1998 (PRELIMINARY) 08, LAST ANNOTATION UPDATE)
 DE SIMILARITY TO A CHOC-CLASS ZINC FINGER
 GN B6432.9
 OS CAENORHABDITIS ELEGANS
 OC EPIKAROTIA METACODA NEMATODA SEPTENTRIONIA PHAROTIA PHAROTIDA
 OC RHABDITIA METACODA NEMATODA SEPTENTRIONIA PHAROTIA PHAROTIDA
 RN 111
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2
 RX MEDLINE: 94150718
 RA WILSON R., ANDERSON K., BAYNES C., BERKS M., BONFIELD J.,
 RA PRITTON T., CONNELL M., DAVIES T., DOWDER J., GUTSON A., GRAYSON M.,
 RA DAVIS J., DAVIES T., DAVIES T., DAVIES T., DAVIES T., DAVIES T.,
 RA HASTING T., HILLIER L., JEFF M., JOHNSON L., JONES M., KERSHAW J.,
 RA KRISTEN J., LASTER N., LATREILLE P., LIGHTNING J., LLOYD C.,
 RA MONTGOMERY A., MONTGOMERY P., MONTGOMERY P., MONTGOMERY P.,
 RA PIERCE L., PIERCE A., PIERCE A., PIERCE A., PIERCE A., PIERCE A.,
 RA SONNHAMMER E., STADEN P., STURTON J., THIEPPE-MIES J., THOMAS K.,
 RA VAUDIN M., VAUGHAN K., WATKINSON P., WATSON A., WEINSTOCK L.,
 RA WILKINSON-SPOAT J., WOLDMAN P.
 RI "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RI elegans." 368132-38(1994).
 RL NATURE 368:32-38(1994).
 RN 121
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2
 RA HENKHAUS J., WOLDMAN P.
 RI SUBMITTED (CAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN 131
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2
 RA WATKINSON P.
 RI SUBMITTED (SEP-1998) TO EMBL/GENBANK/DBJ DATA BANKS
 DR EMBL: 080836, 01207142, 1
 DR PRAM, PROTEIN 7, 080836, 1
 SO SQUIDROTE 127 AA 199808 PRO322

Query Match 3.44 Score 76.5, DB 3, Length 425
 Best Local Similarity 19.74, Pred. No. 22
 Matches 46 Conservative 29 Mismatches 41 Totals 77 Gaps 6

01-NOV-1998 (PRELIMINARY) 08, LAST ANNOTATION UPDATE)
 DE SIMILARITY TO A CHOC-CLASS ZINC FINGER
 GN B6432.9
 OS CAENORHABDITIS ELEGANS
 OC EPIKAROTIA METACODA NEMATODA SEPTENTRIONIA PHAROTIA PHAROTIDA
 OC RHABDITIA METACODA NEMATODA SEPTENTRIONIA PHAROTIA PHAROTIDA
 RN 111
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2
 RX MEDLINE: 94150718
 RA WILSON R., ANDERSON K., BAYNES C., BERKS M., BONFIELD J.,
 RA PRITTON T., CONNELL M., DAVIES T., DOWDER J., GUTSON A., GRAYSON M.,
 RA DAVIS J., DAVIES T., DAVIES T., DAVIES T., DAVIES T., DAVIES T.,
 RA HASTING T., HILLIER L., JEFF M., JOHNSON L., JONES M., KERSHAW J.,
 RA KRISTEN J., LASTER N., LATREILLE P., LIGHTNING J., LLOYD C.,
 RA MONTGOMERY A., MONTGOMERY P., MONTGOMERY P., MONTGOMERY P.,
 RA PIERCE L., PIERCE A., PIERCE A., PIERCE A., PIERCE A., PIERCE A.,
 RA SONNHAMMER E., STADEN P., STURTON J., THIEPPE-MIES J., THOMAS K.,
 RA VAUDIN M., VAUGHAN K., WATKINSON P., WATSON A., WEINSTOCK L.,
 RA WILKINSON-SPOAT J., WOLDMAN P.
 RI "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RI elegans." 368132-38(1994).
 RL NATURE 368:32-38(1994).
 RN 121
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2
 RA HENKHAUS J., WOLDMAN P.
 RI SUBMITTED (CAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN 131
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2
 RA WATKINSON P.
 RI SUBMITTED (SEP-1998) TO EMBL/GENBANK/DBJ DATA BANKS
 DR EMBL: 080836, 01207142, 1
 DR PRAM, PROTEIN 7, 080836, 1
 SO SQUIDROTE 127 AA 199808 PRO322

GenCore version 4.5
Copyright (c) 1993 - 1998 CompuGen Ltd

OM protein : protein search using SW model

Run on: June 22, 1999 11:01:26 Search time: 83.17 Seconds

(without alignments)
104.143 Million cell updates/sec

Title: US-09-030-061-7

Perfect score: 812

Sequence: 1 NGRGHCTAVININQVL KRNENKSWPLTINHS 157

Scoring table: BLOSUM62

Searched: 180763 seqs, 55169189 residues

Database:

SPREMBL.8:
1: sp_fungi:
2: sp_human:
3: sp_invertebrate:
4: sp_mammal:
5: sp_mhc:
6: sp_orfanelle:
7: sp_phase:
8: sp_plant:
9: sp_bacteri:
10: sp_ferment:
11: sp_virus:
12: sp_vertebrate:
13: sp_unclassified:
14: sp_archaea:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
1	739.5	91.1	194	10	088749	088749 ratius norv
2	502	62.7	132	2	075599	075599 homo sapien
3	86	10.6	267	12	073009	073009 gallus gall
4	80	9.9	1196	7	038197	038197 bacterioph
5	80	9.4	1194	9	045916	045916 clostridium
6	80	9.9	1196	9	053550	053550 clostridium
7	79.5	9.8	414	3	024832	024832 elmeria max
8	79.5	9.9	267	4	029082	029082 sus scrofa
9	79	9.7	506	9	084859	084859 chlamydia t
10	78.5	9.7	161	10	062161	062161 mus musculu
11	77	9.6	1146	9	061778	061778 borrelia bu
12	77	9.5	885	10	008759	008759 mus musculu
13	76.5	9.4	866	8	024295	024295 elsum sativ
14	75.5	9.4	1146	9	068317	068317 vibrio chol
15	75.5	9.3	893	2	075283	075283 homo sapien
16	75.1	9.1	729	9	050494	050498 streptomyce
17	74.5	9.2	661	9	073025	073025 synechocyst
18	74	9.1	4410	1	017019	017019 saccharomyc
19	74	9.1	622	2	014859	014859 homo sapien
20	74	9.1	1139	2	016084	016084 homo sapien
21	74	9.1	628	2	013421	013421 homo sapien
22	74	9.1	1139	2	015073	015073 homo sapien
23	74	9.1	1206	1	044194	044194 caenorhabdi
24	74	9.1	1206	2	022177	022177 caenorhabdi
25	74	9.1	254	9	051029	051029 borrelia bu
26	74	9.1	659	14	057721	057721 pyrococcus
27	73	9.0	441	1	005892	005892 saccharomyc
28	73	9.0	779	4	047612	047612 felis silve
29	72	9.0	1248	8	065589	065589 arabidopsis

ALIGNMENTS

30	72.5	8.9	905	1	013955	013955 schizosacch
31	72.5	8.9	690	1	074343	074343 schizosacch
32	72.5	8.9	1466	1	071734	071734 borrelia bu
33	72	8.9	925	2	075986	075986 homo sapien
34	72	8.9	692	2	020447	020447 saccharabdi
35	72	8.9	944	9	080732	080732 arabidopsis
36	72	8.9	797	10	088657	088657 ratius norv
37	71.5	8.8	624	2	054534	054534 chlamydia t
38	71	8.7	868	3	060964	060964 dicystosell
39	71	8.7	270	4	028385	028385 equus caball
40	71	8.7	270	4	077743	077743 equus caball
41	71	8.7	983	8	023511	023511 arabidopsis
42	71	8.7	1230	3	021583	021583 pleurorema
43	71	8.7	1494	9	061391	061391 borrelia bu
44	71	8.7	210	9	094294	094294 bacillus co
45	71	8.7	708	9	033378	033378 nesteria g

RESULT	1
ID	088749
AC	088749
DT	01-NOV-1998 (PREMREPEL 08 CREATED)
DT	01-NOV-1998 (PREMREPEL 08 LAST SEQUENCE UPDATE)
DT	01-NOV-1998 (PREMREPEL 08 LAST ANNOTATION UPDATE)
DE	INTERLEUKIN-18.
GN	IL-18.
OS	PATRUS NORVEGICUS (PAT).
OC	EMKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:
NC	POTENTILLA: SCITROGNATHI: MURINAE: MURINAE: PATIUS:
RN	(1)
RP	SEQUENCE FROM N.A.
PT	STRAIN=SPRAGUE DAWLEY; ISSUES=WHOLE BRAIN;
PA	CHITMAN A.C.; HALL M.D.; POTWELL N.J.; LINESH G.N.;
RT	"Cloning of rat brain interleukin-18 cDNA."
PL	MOL. PSYCH. 3:392-399(1998).
DE	EMBL: A222813; E131519;
PT	CHAIN 134 AA; 194 AA; 123220 UNCLD;
S.	SEQUENCE 134 AA; 194 AA; 123220 UNCLD;

Query Match	91.1%	Score 739.5	DB 10	Length 194
Exact Local Similarity	30.9%	File No. 216-551		
Matches 107	Conservative 11	Mismatches 4	Gaps 1	

QY	1 NGRGHCTAVININQVLNENKSWPLTINHS 157	QY	088749 ratius norv
DB	1 NGRGHCTAVININQVLNENKSWPLTINHS 157	DB	075599 homo sapien
QY	60 AVTLKRGKMSLSTKRNKIIHFMHPPNIGQSNLPPQPVGHKMFESSIVE 119	QY	088749 ratius norv
DB	60 AVTLKRGKMSLSTKRNKIIHFMHPPNIGQSNLPPQPVGHKMFESSIVE 119	DB	075599 homo sapien
QY	97 AVTLKRGKMSLSTKRNKIIHFMHPPNIGQSNLPPQPVGHKMFESSIVE 156	QY	088749 ratius norv
DB	97 AVTLKRGKMSLSTKRNKIIHFMHPPNIGQSNLPPQPVGHKMFESSIVE 156	DB	075599 homo sapien
QY	100 3HLLAQTAVAFVLYLVKLSKSWPLTINHS 157	QY	088749 ratius norv
DB	100 3HLLAQTAVAFVLYLVKLSKSWPLTINHS 157	DB	075599 homo sapien
QY	157 3HLLAQTAVAFVLYLVKLSKSWPLTINHS 154	QY	088749 ratius norv
DB	157 3HLLAQTAVAFVLYLVKLSKSWPLTINHS 154	DB	075599 homo sapien

RESULT	2
ID	075599
AC	075599
DT	01-NOV-1998 (PREMREPEL 08 CREATED)
DT	01-NOV-1998 (PREMREPEL 08 LAST SEQUENCE UPDATE)
DT	01-NOV-1998 (PREMREPEL 08 LAST ANNOTATION UPDATE)
DE	INTERLEUKIN-18 PRECURSOR.
GN	IL18.
OS	HOMO SAPIENS (HUMAN).
OC	EMKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:
NC	PRIMATES: CATARRHINI: HOMININAE: HOMO.

```

DI 01-NOV-1996 (TREMBLER, 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLER, 08, LAST ANNOTATION UPDATE)
DE ANTP-139.
GN ANTP-139.
US BACTERIOPHAGE 1C1.
OC VIRUSES.
RN [1].
RP SEQUENCE FROM N.A.
RC STRAIN-468:
EX MEDLINE, 94301293..
RA HAUSER D F., EKUND M W., BOQUET P., POPOFF M R.:
RT "Organization of the botulinum neurotoxin C1 gene and its associated
EI non-toxic protein genes in Clostridium botulinum C 468."
SI Mol. Gen. Genet. 243:641-649(1994).
SR EMBL, X75722, GI51574.
SO SEQUENCE. 1196 AA; 138725 MW; 6486A4E2 CRC32;

Query Match          9.9% Score 80; DB 7; Length 1196;
Best Local Similarity 24.3%; Pred. No. 65;
Matches 74 Conserving 24 Mismatches 57 Indels 28 Gaps 4

CY 15 TCGASGFEHLILYWKKEVEGLAV--LSVYSKSLISLCKNLTISEMPEN--
LE 968 LSVVSEPLRQTLITF-NRWANVSLESLTSYSTINISLNKNNSNYELSHVNPT 1028
      ||| | | | | | | | | | | | | | | | | | | | | | | | | |
CY 1 -----LQLSCLTFEKAFVGHNNKFESSTLVLLDCKEDAPK 134
DB 1024 TSFVPIINFSYLNSYINDSKSSLSLEYKKNGLYNVFPRIAYE VNNKSY 1 77
CY 134 LLKKDKNGDKSMFTLNLOS 157
DB 1078 LSLKNDGINISSVKFKLINIDES 1101
      ||| | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 5
ID Q45916 PRELIMINARY: PRT: 1194 AA.
AC Q45916;
DI 01-NOV-1996 (TREMBLER, 01, CREATED)
DT 01-NOV-1996 (TREMBLER, 01, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLER, 07, LAST ANNOTATION UPDATE)
DE 138KDA PROTEIN ASSOCIATED WITH BONT /C1-HAEMAGGLUTININ COMPLEX.
GN CHR-138.
OS CLOSTRIDIUM BOTULINUM.
OC VIRIDIBACTERIALES; BACTERIUM; CLOSTRIDIACEAE;
CC CLOSTRIDIUM.
NC [1].
RN RN SEQUENCE FROM N.A.
RP HAUSER D F., EKUND M W., POPOFF M R.:
RA SUBMITTED (MAY-1992) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR EMBL: X66435; GENBANK: U092274; DDBJ:
SQ SEQUENCE 1194 AA; 138725 MW; 019262CA CIRC32;

Query Match          9.9% Score 80; DB 9; Length 1194;
Best Local Similarity 24.3%; Pred. No. 65;
Matches 74 Conserving 24 Mismatches 57 Indels 28 Gaps 4

CY 15 TCGASGFEHLILYWKKEVEGLAV--LSVYSKSLISLCKNLTISEMPEN--
LE 968 LSVVSEPLRQTLITF-NRWANVSLESLTSYSTINISLNKNNSNYELSHVNPT 1028
      ||| | | | | | | | | | | | | | | | | | | | | | | | | |
CY 1 -----LQLSCLTFEKAFVGHNNKFESSTLVLLDCKEDAPK 134
DB 1024 TSFVPIINFSYLNSYINDSKSSLSLEYKKNGLYNVFPRIAYE VNNKSY 1 77
CY 134 LLKKDKNGDKSMFTLNLOS 157
DB 1078 LSLKNDGINISSVKFKLINIDES 1101
      ||| | | | | | | | | | | | | | | | | | | | | | | | | |


```

```

053550
ID 053550 PRELIMINARY: PRT: 1196 AA.
AC 053550
DT 01-NOV-1996 (TEMPREL 01, CREATED)
DT 01-NOV-1996 (TEMPREL 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TEMPREL 02, LAST ANNOTATION UPDATE)
DE PROTEIN TOXIN 1, NONTX101, NONHEMAGGLUTININ COMPONENT (FRAGMENT).
OS CLOSTRIDIUM BOTULINUM
OC BACTERIA, FIRMICUTES, BACILLUS, CLOSTRIDIUM GROUP, CLOSTRIDIACEAE,
OC CLOSTRIDIUM
RN 121
RP SEQUENCE FROM N.A.
RX MEDLINE: 96025415.
RA OHYAMA T., MATSUYAMA T., FUJINAGA Y., INOUE K., SUNAGAWA H., FUJII N.,
RA INOUE K., OGUMA K.
RT "Characterization of nontoxic-nonhemagglutinin component of the two
RT types of Clostridium botulinum toxin (M and L) produced by Clostridium botulinum
RT type D CR-16."
RI Microbiol Immunol 39:457-465(1995)
RL EMBL: S80809, G311691.
FT NON-TER 1196 1196
SC SEQUENCE 1196 AA 119677 MW 6542190 38033

Query Match 9.9% Score 80 DB 9: Length 1196:
Best Local Similarity 24.3% Prod. No. 65:
Matches 24 Conserved 24 Misses 57 Indels 28 Gaps 4

CY 35 INDGASPRGTLIIYKFKSEVGLAV--ILSKSKMSLTKSKNKIIFSEMDPEN-- 91
DB 940 ISIVTFKTLLEFI-NKNNVAVS-TGLTIVSTINISLVKNSIVVEELVLDNPT 1023
CY 91 -----IDQISDLIFPKKPVGSHKNEEESLYSHGLACKEDDAR 133
DB 1024 ISEVINYVESLYDNSTYRQSSKSLDYNNKYOLVYVPEPISLYE-----VNDNNKSY 1077
CY 124 LILKKEENGKSVETLINHOS 157
DB 1078 ISIVTQINISVYKFININER 1101

RESULT 7
024892 PRELIMINARY: PRT: 414 AA.
ID 024892
AC 024892
DT 01-NOV-1996 (TEMPREL 01, CREATED)
DT 01-NOV-1996 (TEMPREL 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TEMPREL 02, LAST ANNOTATION UPDATE)
DE "Anticellulose immunoblotting for identification and molecular gene
DE cloning of Eimeria maxima antigens that stimulate lymphocyte
DE proliferation."
RT Proliferation."
RI Clin Diagn Lab Immunol 2:524-530(1995).
RL 121
RP SEQUENCE FROM N.A.
RX STRAIN-HOUGHTON.
RX MEDLINE: 97048698.
RA DUNN P.J., DUNN P.P.J., TOMLEY F.M.,
RA "Anticellulose immunoblotting for identification of calcium-
RA dependent proteases in Eimeria tenella and Eimeria maxima."
RI Parasitology 113:439-448(1996).
RL EMBL: Z71564, F237260.
FT NON-TER 414 414
SC SEQUENCE 414 AA 108717 MW 6542190 38033

DR PFAM: PF00036, ehand, 4.
DR PFAM: PF00065, pkinase, 1.
FT NON-TER 1

```

```

SU SEQUENCE 414 AA: 17427 MW, 4287169 09022:
Query Match 9.9% Score 79.5 DB 9: Length 414:
Best Local Similarity 25.7% Prod. No. 20:
Matches 24 Conserved 22 Misses 40 Indels 21 Gaps 4

CY 42 PPTPLIYKKEVGLA...VLSVDS...KXSTISCKKXIFSEMDPEN 91
DB 174 PMPVVFPAKLIIPMLVVFPMISAKVLDHFWIPISTVAVDSI-----NL 223
CY 92 DQSGSIFPKKPVGSHKNEEESLYSHGLACKEDDAPLTKKRESD 144
DB 224 PSEFTSTIN-PPTGCTTAAALTYVSKLTIELIELNKILFPMKSD 275

RESULT 8
029082 PRELIMINARY: PRT: 267 AA.
ID 029082
AC 029082
DT 01-NOV-1996 (TEMPREL 01, CREATED)
DT 01-NOV-1996 (TEMPREL 02, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TEMPREL 02, LAST ANNOTATION UPDATE)
DE INTERLEUKIN 1-BETA.
OS SUS SCROFA (PIG).
RA EKARVATA, METRICA, CHRODATA, VERTEBRATA, MAMMALIA, EUTHERIA,
RA ARTIODACTYLA, SUINAE, SUIA, SUIDAE, SUI.
RN 121
RP SEQUENCE FROM N.A.
RX TISSUE=LIVER.
RX MEDLINE: 94039070.
RA VANDERKROEK K., PIEN P., BEKEN E., MARTENS E., JANSSEN A.,
RA VAN DAMME J., OPDENAKKER G., BILLAU A.
RT "Gene expression, RNA stability, and expression in E. coli and
RT genetically altered host cells: expression of porcine interleukin 1 beta."
RI EMBL: X74564, G407900.
FT PROSITE: PS0253, INTERLEUKIN 1.
DR PFAM: PF00340, interleukin-1.
SC SEQUENCE 267 AA 10894 MW 6542190 38033

Query Match 9.9% Score 79.5 DB 4: Length 267:
Best Local Similarity 25.6% Prod. No. 12:
Matches 24 Conserved 22 Misses 40 Indels 21 Gaps 4

CY 53 DSEVGLAVTISKESMSLTKSKNK---ISFEMD---PENIDTSGHIFPKRV 105
DB 165 DSEVGLAVTISKESMSLTKSKNK---ISFEMD---PENIDTSGHIFPKRV 105
CY 106 FQNKKEEESLYSHGLACKED 129
DB 221 --KRVFESALTYMVISQAF 242

RESULT 9
084869 PRELIMINARY: PRT: 506 AA.
ID 084869
AC 084869
DT 01-NOV-1996 (TEMPREL 08, CREATED)
DT 01-NOV-1996 (TEMPREL 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TEMPREL 16, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 58.5 KD PROTEIN.
CN C8861.
OS CHLAMYDIA TRACHOMATIS.
OC BACTERIA, CHLAMYDIALES, CHLAMYDIACEAE, CHLAMYDIA.
RN 121
RP SEQUENCE FROM N.A.

```


Wed Jun 23 09:59:19 1999

STAIN=STAIN X 74.
 RA HAIRKAYAMA S, JENSEN J P, WEISSMAN A M :
 "Subcellular localization and ubiquitin-conjugating enzyme (E2) interactions of mammalian HECT family ubiquitin protein ligases."
 J. BIOL. CHEM. 273:15062-15072(1997).
 RA KUROTA T, CHRISTIAN S L, PRESSLER J, CATTANACH B, LEDBETTER D H, BEADLER A L :
 "The E6-AP ubiquitin-protein ligase (UBE3A) gene is localized within a narrow Angelman syndrome critical region."
 GENOME RES. 7:368-377(1997).
 CC - FUNCTION: INTERACTS WITH THE E6 PROTEIN OF THE CANCER-ASSOCIATED HUMAN PAPILLOMAVIRUS TYPES 16 AND 18. THE E6/E6-AP COMPLEX BINDS TO AND TARGETS THE E2 TYPE SUPPRESSOR PROTEIN FOR URICITIN-MEDIATED PROTEOLYSIS. E6-AP IS AN E3 URICITIN-PROTEIN LIGASE WHICH ACCEPTS URICITIN FROM AN E2 URICITIN-CONUGATING ENZYME IN THE FORM OF A THIOESTER AND THEN DIRECTLY TRANSFERS THE URICITIN TO TARGETED SUBSTRATES.
 CC - SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC
 CC - TISSUE SPECIFICITY: MOST ABUNDANT IN BRAIN, HEART AND THYMUS.
 CC - A CYSTEINE RESIDUE IS REQUIRED FOR URICITIN-THIOESTER FORMATION.
 CC - SIMILARITY: CONTAINS AN HECT-TYPE E3 URICITIN-PROTEIN LIGASE DOMAIN.
 CC - CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-38 IS THE INITIATOR
 DR EMBL: U66636: G209625 :
 DR EMBL: U62122: 5183527 :
 DR M30: M3105098: UBE3A.
 DR PRAM: PR06633: HECT-1
 KM NUCLEAR PROTEIN; URICITIN CONUGATING; LIGASE.
 FI DOMAIN 405 410
 FI BINDING 786 885
 FI CONFLICT 853 853 HECT DOMAIN.
 FI CONFLICT 197 197 URICITIN (BY SIMILARITY).
 FI CONFLICT 301 301 D -> E (IN REF. 2).
 FI CONFLICT 343 343 T -> V (IN REF. 2).
 FI CONFLICT 394 394 N -> S (IN REF. 2).
 FI CONFLICT 450 450 S -> F (IN REF. 2).
 FI CONFLICT 486 486 G -> F (IN REF. 2).
 FI CONFLICT 525 525 T -> P (IN REF. 2).
 FI CONFLICT 577 577 DEPTVS -> MEAREP (IN REF. 2).
 FI CONFLICT 584 584 E -> S (IN REF. 2).
 FI CONFLICT 587 588 G -> S (IN REF. 2).
 FI CONFLICT 597 597 T -> N (IN REF. 2).
 FI CONFLICT 627 627 FTLLG -> VVSDWH (IN REF. 2).
 FI CONFLICT 725 725 IS -> NL (IN REF. 2).
 FI CONFLICT 817 817 L -> Q (IN REF. 2).
 FI CONFLICT 869 870 NV -> KE (IN REF. 2).
 SQ SEQUENCE 885 AA: 101175 MW: 5260163 CP:322:

Query Match 9.5% Score 77: DB 10: Length 885:
 Best Local Similarity 26.7%: Prol No 80:
 Matches 31: Conservative 20: Mismatches 35: Indels 30: Gaps 7:

QY 14 NMTNVIYVQPPVNF--NMTHNQASFPQPLIYWKSEVYVGLAVTISYDQKMS 71
 DB 402 NHEF-----EFTTFSEETLGLDGLGFFFNK-----KGFVDFLETELVG----- 447
 DB 447 TLNRPPLISFESINELPNIIVIMKNTVF-----KVTEN---KGSFMTG 491

RESULT 13
 024295
 IF 024295
 AC 024295
 EFFITIMAFY PFT 866 AA

QY 01-JAN-1998 (TREMURPEL 05, CREATED)
 DT 01-JAN-1998 (TREMURPEL 05, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMURPEL 08, LAST ANNOTATION UPDATE)
 DE LIPOXYGENASE.
 GN LOX1PS55.
 OS PISUM SATIVUM (GARDEN PEA).
 CC EUKARYOTA, VIRIDIPHYTA, CHLADOPHYTA/EMPHYPHYTA GROUP, EUPHYPHYTA;
 CC ICHAEOPHYTA: EUPHYPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA;
 CC EUDICOTYLEDONS: POSITAF: FABALES: FABACEAE: PAPILLIONOIDEAE: PISUM.
 RN [1]
 RP SEQUENCE FROM N.A.
 PC STRAIN=CV, BIRTE;
 RA FORSTER C.;
 RL SUBMITTED (NW-1997) TO EMBL/GENBANK/DEED DATA BANKS.
 DR EMBL: Y15410: E117502 :
 DR PROSITE: PS00981: LIPOXYGENASE_2: 1:
 DR PROSITE: PS00711: LIPOXYGENASE_1: 1:
 DR PRAM: PR00305: Lipoxigenase: 1:
 SQ SEQUENCE 866 AA: 97748 MW: 97309315 CP:322.

Query Match 9.4% Score 76.5: DB 6: Length 866:
 Best Local Similarity 21.5%: Prol No 86:
 Matches 40: Conservative 29: Mismatches 46: Indels 21: Gaps 8:

QY 1 NPSLFTTAVININQVIFV--EKPQPFEMTITQASSEPQPIIYWKSEVPA 59
 DB 419 NLSL-----EVAVANN--EPLILYHAPILYINKNAKAAALILFELDGLSTKL 474
 QY 60 AVLTISV-----KSKN-----STL-----SKNKIIF----- 93
 DB 475 ALESLHPSGQVSLSEVILFLDQGVSTILSLKAVIVDSYHOLNSWMLHAY 514
 QY 92 -----EEMF-----EENL-----LSEALFETKVIYKEMEF 123
 DB 535 VEPHIANHNVSVHPIPLLPHPITINISLAPALINAGIIEQPLPQSSVPM 594
 QY 114 ESLEYE 119
 DB 595 SSAYK 600

RESULT 14
 068317
 ID 068317: PFEIMINARY. PFT, 1146 AA.
 DT 01-NOV-1998 (TREMURPEL 07, CREATED)
 DT 01-NOV-1998 (TREMURPEL 07, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMURPEL 08, LAST ANNOTATION UPDATE)
 DE SENSOR KINASE.
 GN VIES.
 OS VIRIDIO CHLADOPHYTA
 CC BACTERIA: PROTEOBACTERIA: GAMMA SIBDIVISION: VIBRIONACEAE: VIBRIO.
 RN [1]
 RP SEQUENCE FROM N.A.
 PC STRAIN=C6709-1, EL TOP;
 RX MEDLINE: 98323722.
 RA LEE S H, ANGELICHO M J, MEKALANOS J J, CAMILLI A :
 "Nucleotide sequence and spatiotemporal expression of the Vibrio cholerae viesAB genes during infection."
 J. BACTERIO. 180:3296-3305(1998)
 DR EMBL: AF031552: G3123890 :
 SQ SEQUENCE 1146 AA: 129484 MW: 2160036 CP:322:

Query Match 9.4% Score 76.5: DB 6: Length 1146:
 Best Local Similarity 23.4%: Prol No 126:02:
 Matches 33: Conservative 25: Mismatches 50: Indels 21: Gaps 9:

QY 31 DMTITDQASEP--QTEPI---IYWKSEVYVGLAVTISYDQKMSILSKNLIISHEMD 86
 DB 862 EVSNILAQITFASPSGQVSLSEVILFLDQGVSTILSLKAVIVDSYHOLNSWMLHAY 514

